

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Summers, Neena
McWherter, Charles
Feng, Yiqing

(ii) TITLE OF THE INVENTION: Novel Erythropoietin Receptor Agonists

(iii) NUMBER OF SEQUENCES: 134

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: G. D. Searle & Co.
(B) STREET: P.O. Box 5110
(C) CITY: Chicago
(D) STATE: IL
(E) COUNTRY: U. S. A.
(F) ZIP: 60680

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 21-OCT-1997
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/034,044
(B) FILING DATE: 25-OCT-1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Bennett, Dennis A
(B) REGISTRATION NUMBER: 34,547
(C) REFERENCE/DOCKET NUMBER: 2991/1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 314-737-6986
(B) TELEFAX: 314-737-6972
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Asn | Ile | Thr | Thr | Gly | Cys | Ala | Glu | His | Cys | Ser | Leu | Asn | Glu | Asn | Ile |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | |
| Thr | Val | Pro | Asp | Thr | Lys | Val | Asn | Phe | Tyr | Ala | Trp | Lys | Arg | Met | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Gly | Gln | Gln | Ala | Val | Glu | Val | Trp | Gln | Gly | Leu | Ala | Leu | Leu | Ser |
| | | | 35 | | | | | 40 | | | | | 45 | | |
| Glu | Ala | Val | Leu | Arg | Gly | Gln | Ala | Leu | Leu | Val | Asn | Ser | Ser | Gln | Pro |
| | | | 50 | | | | 55 | | | | 60 | | | | |
| Trp | Glu | Pro | Leu | Gln | Leu | His | Val | Asp | Lys | Ala | Val | Ser | Gly | Leu | Arg |
| | | | 65 | | | | 70 | | | 75 | | | | 80 | |
| Ser | Leu | Thr | Thr | Leu | Leu | Arg | Ala | Leu | Gly | Ala | Gln | Lys | Glu | Ala | Ile |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Ser | Pro | Pro | Asp | Ala | Ala | Ser | Ala | Ala | Pro | Leu | Arg | Thr | Ile | Thr | Ala |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Asp | Thr | Phe | Arg | Lys | Leu | Phe | Arg | Val | Tyr | Ser | Asn | Phe | Leu | Arg | Gly |

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SECRET 46646680

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      115      120      125
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly
      130      135      140
Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
145      150      155
Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
      165      170

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr
 1      5      10      15
Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val
      20      25      30
Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Ser Glu
      35      40      45
Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp
50      55      60
Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser
65      70      75
Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
      85      90      95
Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp
100      105      110
Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys
      115      120      125
Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly
130      135      140
Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
145      150      155
Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn
      165      170

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
 1      5      10      15
Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
      20      25      30
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
      35      40      45
Val Leu Arg Gly Gln Ala Leu Val Asn Ser Ser Gln Pro Trp Glu
50      55      60
Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
65      70      75
Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro
      85      90      95
Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr
100      105      110
Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu
      115      120      125
Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly
130      135      140
Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr
145      150      155
Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
      165      170

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ala | Glu | His | Cys | Ser | Leu | Asn | Glu | Asn | Ile | Thr | Val | Pro | Asp | Thr |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Lys | Val | Asn | Phe | Tyr | Ala | Trp | Lys | Arg | Met | Glu | Val | Gly | Gln | Gln | Ala |
| | | 20 | | | | | 25 | | | | | 30 | | | |
| Val | Glu | Val | Trp | Gln | Gly | Leu | Ala | Leu | Leu | Ser | Glu | Ala | Val | Leu | Arg |
| | 35 | | | | 40 | | | | | | 45 | | | | |
| Gly | Gln | Ala | Leu | Leu | Val | Asn | Ser | Ser | Gln | Pro | Trp | Glu | Pro | Leu | Gln |
| | 50 | | | 55 | | | | | 60 | | | | | | |
| Leu | His | Val | Asp | Lys | Ala | Val | Ser | Gly | Leu | Arg | Ser | Leu | Thr | Thr | Leu |
| 65 | | | 70 | | | | | 75 | | | | | | 80 | |
| Leu | Arg | Ala | Leu | Gly | Ala | Gln | Lys | Glu | Ala | Ile | Ser | Pro | Pro | Asp | Ala |
| | | 85 | | | | | | 90 | | | | | | 95 | |
| Ala | Ser | Ala | Ala | Pro | Leu | Arg | Thr | Ile | Thr | Ala | Asp | Thr | Phe | Arg | Lys |
| | | 100 | | | | | 105 | | | | | | 110 | | |
| Leu | Phe | Arg | Val | Tyr | Ser | Asn | Phe | Leu | Arg | Gly | Lys | Leu | Lys | Leu | Tyr |
| | 115 | | | | 120 | | | | | | 125 | | | | |
| Thr | Gly | Glu | Ala | Cys | Arg | Thr | Gly | Asp | Arg | Gly | Gly | Gly | Ser | Ala | Pro |
| | 130 | | | 135 | | | | 140 | | | | | | | |
| Pro | Arg | Leu | Ile | Cys | Asp | Ser | Arg | Val | Leu | Glu | Arg | Tyr | Leu | Leu | Glu |
| 145 | | | 150 | | | | | 155 | | | | | | | 160 |
| Ala | Lys | Glu | Ala | Glu | Asn | Ile | Thr | Thr | Gly | | | | | | |
| | | | 165 | | | | | 170 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Glu | His | Cys | Ser | Leu | Asn | Glu | Asn | Ile | Thr | Val | Pro | Asp | Thr | Lys |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | |
| Val | Asn | Phe | Tyr | Ala | Trp | Lys | Arg | Met | Glu | Val | Gly | Gln | Gln | Ala | Val |
| | | 20 | | | | | 25 | | | | | 30 | | | |
| Glu | Val | Trp | Gln | Gly | Leu | Ala | Leu | Ser | Glu | Ala | Val | Leu | Arg | Gly | |
| | 35 | | | | 40 | | | | | | 45 | | | | |
| Gln | Ala | Leu | Leu | Val | Asn | Ser | Gln | Pro | Trp | Glu | Pro | Leu | Gln | Leu | |
| | 50 | | | 55 | | | | 60 | | | | | | | |
| His | Val | Asp | Lys | Ala | Val | Ser | Gly | Leu | Arg | Ser | Leu | Thr | Thr | Leu | Leu |
| 65 | | | 70 | | | | | 75 | | | | | | 80 | |
| Arg | Ala | Leu | Gly | Ala | Gln | Lys | Glu | Ala | Ile | Ser | Pro | Pro | Asp | Ala | Ala |
| | | 85 | | | | | | 90 | | | | | | 95 | |
| Ser | Ala | Ala | Pro | Leu | Arg | Thr | Ile | Thr | Ala | Asp | Thr | Phe | Arg | Lys | Leu |
| | | 100 | | | | | 105 | | | | | 110 | | | |
| Phe | Arg | Val | Tyr | Ser | Asn | Phe | Leu | Arg | Gly | Lys | Leu | Lys | Leu | Tyr | Thr |
| | 115 | | | | 120 | | | | | | 125 | | | | |
| Gly | Glu | Ala | Cys | Arg | Thr | Gly | Asp | Arg | Gly | Gly | Gly | Ser | Ala | Pro | Pro |
| | 130 | | | | 135 | | | | 140 | | | | | | |
| Arg | Leu | Ile | Cys | Asp | Ser | Arg | Val | Leu | Glu | Arg | Tyr | Leu | Leu | Glu | Ala |
| 145 | | | 150 | | | | | 155 | | | | | | | 160 |
| Lys | Glu | Ala | Glu | Asn | Ile | Thr | Thr | Gly | Cys | | | | | | |
| | | | 165 | | | | | 170 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|----|-----|-----|
| 1 | Asn | Phe | Tyr | Ala | 5 | Trp | Lys | Arg | Met | 10 | Glu | Val | Gly | Gln | Gln | Ala | 15 | Val | Glu |
| | | | | 20 | | | | | | 25 | | | | | | 30 | | | |
| Val | Trp | Gln | Gly | Leu | Ala | Leu | Leu | Leu | Ser | Glu | Ala | Val | Leu | Arg | Gly | Gln | | | |
| | | 35 | | | | | | 40 | | | | | | 45 | | | | | |
| Ala | Leu | Leu | Val | Asn | Ser | Ser | Gln | Pro | Trp | Glu | Pro | Leu | Gln | Leu | His | | | | |
| | 50 | | | | 55 | | | | | 60 | | | | | | | | | |
| Val | Asp | Lys | Ala | Val | Ser | Gly | Leu | Arg | Ser | Leu | Thr | Thr | Leu | Leu | Arg | | | | |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 | | | | |
| Ala | Leu | Gly | Ala | Gln | Lys | Glu | Ala | Ile | Ser | Pro | Pro | Asp | Ala | Ala | Ser | | | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | | | |
| Ala | Ala | Pro | Leu | Arg | Thr | Ile | Thr | Ala | Asp | Thr | Phe | Arg | Lys | Leu | Phe | | | | |
| | | 100 | | | | | | 105 | | | | | | 110 | | | | | |
| Arg | Val | Tyr | Ser | Asn | Phe | Leu | Arg | Gly | Lys | Leu | Lys | Leu | Tyr | Thr | Gly | | | | |
| | | 115 | | | | | 120 | | | | | | 125 | | | | | | |
| Glu | Ala | Cys | Arg | Thr | Gly | Asp | Arg | Gly | Gly | Gly | Ser | Ala | Pro | Pro | Arg | | | | |
| | 130 | | | | 135 | | | | | | 140 | | | | | | | | |
| Leu | Ile | Cys | Asp | Ser | Arg | Val | Leu | Glu | Arg | Tyr | Leu | Leu | Glu | Ala | Lys | | | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | | | |
| Glu | Ala | Glu | Asn | Ile | Thr | Thr | Gly | Cys | Ala | | | | | | | | | | |
| | | | | 165 | | | | | 170 | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| His | Cys | Ser | Leu | Asn | Glu | Asn | Ile | Thr | Val | Pro | Asp | Thr | Lys | Val | Asn |
| 1 | | | | 5 | | | | | 10 | | | | 15 | | |
| Phe | Tyr | Ala | Trp | Lys | Arg | Met | Glu | Val | Gly | Gln | Gln | Ala | Val | Glu | Val |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Trp | Gln | Gly | Leu | Ala | Leu | Leu | Ser | Glu | Ala | Val | Leu | Arg | Gly | Gln | Ala |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Leu | Val | Asn | Ser | Ser | Gln | Pro | Trp | Glu | Pro | Leu | Gln | Leu | His | Val |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| Asp | Lys | Ala | Val | Ser | Gly | Leu | Arg | Ser | Leu | Thr | Thr | Leu | Leu | Arg | Ala |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Leu | Gly | Ala | Gln | Lys | Glu | Ala | Ile | Ser | Pro | Pro | Asp | Ala | Ala | Ser | Ala |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Ala | Pro | Leu | Arg | Thr | Ile | Thr | Ala | Asp | Thr | Phe | Arg | Lys | Leu | Phe | Arg |
| | | 100 | | | | | | 105 | | | | | 110 | | |
| Val | Tyr | Ser | Asn | Phe | Leu | Arg | Gly | Lys | Leu | Lys | Leu | Tyr | Thr | Gly | Glu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ala | Cys | Arg | Thr | Gly | Asp | Arg | Gly | Gly | Gly | Ser | Ala | Pro | Pro | Arg | Leu |
| | 130 | | | | 135 | | | | | 140 | | | | | |
| Ile | Cys | Asp | Ser | Arg | Val | Leu | Glu | Arg | Tyr | Leu | Leu | Glu | Ala | Lys | Glu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ala | Glu | Asn | Ile | Thr | Thr | Gly | Cys | Ala | Glu | | | | | | |
| | | | | 165 | | | | | 170 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Ser | Leu | Asn | Glu | Asn | Ile | Thr | Val | Pro | Asp | Thr | Lys | Val | Asn | Phe |
| 1 | | | | 5 | | | | | 10 | | | | 15 | | |
| Tyr | Ala | Trp | Lys | Arg | Met | Glu | Val | Gly | Gln | Gln | Ala | Val | Glu | Val | Trp |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Gln | Gly | Leu | Ala | Leu | Leu | Ser | Glu | Ala | Val | Leu | Arg | Gly | Gln | Ala | Leu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Leu | Val | Asn | Ser | Ser | Gln | Pro | Trp | Glu | Pro | Leu | Gln | Leu | His | Val | Asp |
| | 50 | | | | | 55 | | | | | 60 | | | | |

```

Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
65      70      75      80
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
85      90      95
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
100      105      110
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
115      120      125
Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile
130      135      140
Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala
145      150      155      160
Glu Asn Ile Thr Thr Gly Cys Ala Glu His
165      170

```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr
1      5      10      15
Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln
20      25      30
Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
35      40      45
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys
50      55      60
Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
65      70      75      80
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro
85      90      95
Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr
100      105      110
Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys
115      120      125
Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys
130      135      140
Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
145      150      155      160
Asn Ile Thr Thr Gly Cys Ala Glu His Cys
165      170

```

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala
1      5      10      15
Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly
20      25      30
Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val
35      40      45
Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
50      55      60
Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala
65      70      75      80
Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu
85      90      95
Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser
100      105      110
Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg

```

```

      115              120              125
Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp
      130              135              140
Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn
145              150              155
Ile Thr Thr Gly Cys Ala Glu His Cys Ser
      165              170

```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

```

Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp
 1              5              10              15
Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu
      20              25              30
Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Val Asn
      35              40              45
Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val
50              55              60
Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln
65              70              75              80
Lys Glu Ala Ile Ser Pro Pro Asp Ala Ser Ala Ala Pro Leu Arg
      85              90              95
Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn
      100              105              110
Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr
      115              120              125
Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser
130              135              140
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
145              150              155              160
Thr Thr Gly Cys Ala Glu His Cys Ser Leu
      165              170

```

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

```

Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
 1              5              10              15
Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
      20              25              30
Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser
      35              40              45
Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
50              55              60
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys
65              70              75              80
Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
      85              90              95
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe
      100              105              110
Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
      115              120              125
Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg
130              135              140
Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr
145              150              155              160
Thr Gly Cys Ala Glu His Cys Ser Leu Asn
      165              170

```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```

Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 1          5          10          15
Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 20          25          30
Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 35          40          45
Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 50          55          60
Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 65          70          75          80
Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
 85          90          95
Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
100          105          110
Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
115          120          125
Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val
130          135          140
Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
145          150          155          160
Gly Cys Ala Glu His Cys Ser Leu Asn Glu
165          170

```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```

Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met
 1          5          10          15
Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
 20          25          30
Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln
 35          40          45
Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu
 50          55          60
Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala
 65          70          75          80
Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr
 85          90          95
Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
100          105          110
Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
115          120          125
Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu
130          135          140
Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly
145          150          155          160
Cys Ala Glu His Cys Ser Leu Asn Glu Asn
165          170

```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Asp | Thr | Lys | Val | Asn | Phe | Tyr | Ala | Trp | Lys | Arg | Met | Glu | Val |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gly | Gln | Gln | Ala | Val | Glu | Val | Trp | Gln | Gly | Leu | Ala | Leu | Leu | Ser | Glu |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Ala | Val | Leu | Arg | Gly | Gln | Ala | Leu | Val | Asn | Ser | Ser | Gln | Pro | Trp | |
| | | 35 | | | | | 40 | | | | 45 | | | | |
| Glu | Pro | Leu | Gln | Leu | His | Val | Asp | Lys | Ala | Val | Ser | Gly | Leu | Arg | Ser |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| Leu | Thr | Thr | Leu | Leu | Arg | Ala | Leu | Gly | Ala | Gln | Lys | Glu | Ala | Ile | Ser |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Pro | Pro | Asp | Ala | Ala | Ser | Ala | Ala | Pro | Leu | Arg | Thr | Ile | Thr | Ala | Asp |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Thr | Phe | Arg | Lys | Leu | Phe | Arg | Val | Tyr | Ser | Asn | Phe | Leu | Arg | Gly | Lys |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Leu | Lys | Leu | Tyr | Thr | Gly | Glu | Ala | Cys | Arg | Thr | Gly | Asp | Arg | Gly | Gly |
| | | 115 | | | | 120 | | | | | | 125 | | | |
| Gly | Ser | Ala | Pro | Pro | Arg | Leu | Ile | Cys | Asp | Ser | Arg | Val | Leu | Glu | Arg |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Tyr | Leu | Leu | Glu | Ala | Lys | Glu | Ala | Glu | Asn | Ile | Thr | Thr | Gly | Cys | Ala |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Glu | His | Cys | Ser | Leu | Asn | Glu | Asn | Ile | Thr | | | | | | |
| | | | | 165 | | | | 170 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Pro | Asp | Thr | Lys | Val | Asn | Phe | Tyr | Ala | Trp | Lys | Arg | Met | Glu | Val | Gly |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Gln | Gln | Ala | Val | Glu | Val | Trp | Gln | Gly | Leu | Ala | Leu | Leu | Ser | Glu | Ala |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Val | Leu | Arg | Gly | Gln | Ala | Leu | Leu | Val | Asn | Ser | Ser | Gln | Pro | Trp | Glu |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Pro | Leu | Gln | Leu | His | Val | Asp | Lys | Ala | Val | Ser | Gly | Leu | Arg | Ser | Leu |
| | 50 | | | | 55 | | | | | 60 | | | | | |
| Thr | Thr | Leu | Leu | Arg | Ala | Leu | Gly | Ala | Gln | Lys | Glu | Ala | Ile | Ser | Pro |
| 65 | | | | 70 | | | | | | 75 | | | | | 80 |
| Pro | Asp | Ala | Ala | Ser | Ala | Ala | Pro | Leu | Arg | Thr | Ile | Thr | Ala | Asp | Thr |
| | | | 85 | | | | | 90 | | | | | | 95 | |
| Phe | Arg | Lys | Leu | Phe | Arg | Val | Tyr | Ser | Asn | Phe | Leu | Arg | Gly | Lys | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Lys | Leu | Tyr | Thr | Gly | Glu | Ala | Cys | Arg | Thr | Gly | Asp | Arg | Gly | Gly | Gly |
| | | 115 | | | | 120 | | | | | | 125 | | | |
| Ser | Ala | Pro | Pro | Arg | Leu | Ile | Cys | Asp | Ser | Arg | Val | Leu | Glu | Arg | Tyr |
| | | 130 | | | | 135 | | | | | 140 | | | | |
| Leu | Leu | Glu | Ala | Lys | Glu | Ala | Glu | Asn | Ile | Thr | Thr | Gly | Cys | Ala | Glu |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| His | Cys | Ser | Leu | Asn | Glu | Asn | Ile | Thr | Val | | | | | | |
| | | | | 165 | | | | 170 | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln

```

      1           5           10           15
Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val
      20           25           30
Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
      35           40           45
Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr
      50           55           60
Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro
      65           70           75           80
Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
      85           90           95
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys
      100          105          110
Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser
      115          120          125
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
      130          135          140
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
      145          150          155          160
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
      165          170

```

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

```

Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
      1           5           10           15
Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser
      20           25           30
Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
      35           40           45
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys
      50           55           60
Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
      65           70           75           80
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe
      85           90           95
Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
      100          105          110
Asp Arg Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg
      115          120          125
Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr
      130          135          140
Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
      145          150          155          160
Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
      165          170

```

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

```

Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
      1           5           10           15
Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
      20           25           30
Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
      35           40           45
Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
      50           55           60

```

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
65 70 75 80
Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
85 90 95
Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
100 105 110
Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val
115 120 125
Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
130 135 140
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp
145 150 155 160
Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
165 170

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
1 5 10 15
Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln
20 25 30
Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu
35 40 45
Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala
50 55 60
Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr
65 70 75 80
Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
85 90 95
Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
100 105 110
Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu
115 120 125
Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly
130 135 140
Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr
145 150 155 160
Lys Val Asn Phe Tyr Ala Trp Lys Arg Met
165 170

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser
1 5 10 15
Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro
20 25 30
Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg
35 40 45
Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile
50 55 60
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
65 70 75 80
Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
85 90 95
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly
100 105 110
Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu

```

      115              120              125
Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
   130              135              140
Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
   145              150              155
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu
      165              170

```

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu
 1      5      10      15
His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
   20      25      30
Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala
   35      40      45
Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu
   50      55      60
Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr
   65      70      75      80
Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro
   85      90      95
Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
  100     105     110
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu
  115     120     125
Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp
  130     135     140
Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu
  145     150     155     160
Ala Leu Leu Ser Glu Ala Val Leu Arg Gly
      165      170

```

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His
 1      5      10      15
Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
   20      25      30
Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser
   35      40      45
Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe
   50      55      60
Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly
   65      70      75      80
Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg
   85      90      95
Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys
  100     105     110
Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn
  115     120     125
Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
  130     135     140
Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
  145     150     155     160
Leu Leu Ser Glu Ala Val Leu Arg Gly Gln
      165      170

```

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

```

Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val
 1      5      10      15
Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala
 20      25      30
Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala
 35      40      45
Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg
 50      55      60
Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu
 65      70      75      80
Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu
 85      90      95
Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
100      105      110
Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
115      120      125
Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
130      135      140
Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
145      150      155      160
Leu Ser Glu Ala Val Leu Arg Gly Gln Ala
165      170

```

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```

Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
 1      5      10      15
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
 20      25      30
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
 35      40      45
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 50      55      60
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
 65      70      75      80
Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile
 85      90      95
Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala
100      105      110
Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
115      120      125
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met
130      135      140
Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
145      150      155      160
Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
165      170

```

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```

Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys
 1      5      10      15
Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
      20      25      30
Ala Gln Lys Glu Ala Ile Ser Pro Asp Ala Ala Ser Ala Ala Pro
      35      40      45
Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr
      50      55      60
Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys
      65      70      75      80
Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys
      85      90      95
Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
      100      105      110
Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile
      115      120      125
Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu
      130      135      140
Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser
      145      150      155      160
Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
      165      170

```

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

```

Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
 1      5      10      15
Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala
      20      25      30
Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu
      35      40      45
Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser
      50      55      60
Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg
      65      70      75      80
Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp
      85      90      95
Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn
      100      105      110
Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr
      115      120      125
Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val
      130      135      140
Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu
      145      150      155      160
Ala Val Leu Arg Gly Gln Ala Leu Leu Val
      165      170

```

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

```

Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val

```

```

1          5          10          15
Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln
20          25          30
Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg
35          40          45
Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn
50          55          60
Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr
65          70          75
Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser
85          90          95
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
100          105          110
Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
115          120          125
Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
130          135          140
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
145          150          155          160
Val Leu Arg Gly Gln Ala Leu Leu Val Asn
165          170

```

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```

Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
1          5          10          15
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys
20          25          30
Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
35          40          45
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe
50          55          60
Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
65          70          75
Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg
85          90          95
Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr
100          105          110
Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
115          120          125
Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln
130          135          140
Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val
145          150          155          160
Leu Arg Gly Gln Ala Leu Leu Val Asn Ser
165          170

```

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
1          5          10          15
Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
20          25          30
Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
35          40          45
Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
50          55          60

```

```

Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
65      70      75      80
Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val
      85      90      95
Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
      100      105      110
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp
      115      120      125
Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln
      130      135      140
Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu
145      150      155      160
Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
      165      170

```

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu
1      5      10      15
Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala
      20      25      30
Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr
      35      40      45
Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
50      55      60
Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
65      70      75      80
Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu
      85      90      95
Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly
      100      105      110
Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr
      115      120      125
Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
      130      135      140
Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
145      150      155      160
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln
      165      170

```

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```

Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg
1      5      10      15
Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile
      20      25      30
Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
      35      40      45
Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
50      55      60
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly
65      70      75      80
Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
      85      90      95
Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
      100      105      110
Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys

```



```

      115              120              125
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val
      130              135              140
Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly
145              150              155
Gln Ala Leu Leu Val Asn Ser Ser Gln Pro
      165              170

```

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser
 1      5      10      15
Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
      20      25      30
Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp
      35      40      45
Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys
50      55      60
Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly
65      70      75      80
Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg
      85      90      95
Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala
      100      105      110
Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val
      115      120      125
Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu
130      135      140
Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln
145      150      155
Ala Leu Leu Val Asn Ser Ser Gln Pro Trp
      165      170

```

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala
 1      5      10      15
Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys
      20      25      30
Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
      35      40      45
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro
50      55      60
Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu
65      70      75      80
Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser
      85      90      95
Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala
      100      105      110
Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly
      115      120      125
Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val
130      135      140
Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
145      150      155
Val Ser Gly Leu Arg Ser Leu Thr Thr Leu
      165      170

```

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala
 1      5      10      15
Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu
      20      25      30
Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr
      35      40      45
Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro
      50      55      60
Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
65      70      75      80
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu
      85      90      95
Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp
      100      105      110
Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu
      115      120      125
Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn
      130      135      140
Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val
145      150      155      160
Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
      165      170

```

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

```

Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser
 1      5      10      15
Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe
      20      25      30
Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly
      35      40      45
Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg
      50      55      60
Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys
65      70      75      80
Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn
      85      90      95
Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
      100      105      110
Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
      115      120      125
Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser
      130      135      140
Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
145      150      155      160
Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg
      165      170

```

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala
 1      5      10      15
Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg
      20      25      30
Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu
      35      40      45
Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu
      50      55      60
Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
65      70      75      80
Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
      85      90      95
Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
      100      105      110
Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
      115      120      125
Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
      130      135      140
Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
145      150      155      160
Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala
      165      170

```

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

```

Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
 1      5      10      15
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
      20      25      30
Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
      35      40      45
Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile
      50      55      60
Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala
65      70      75      80
Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
      85      90      95
Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met
      100      105      110
Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
      115      120      125
Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln
      130      135      140
Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu
145      150      155      160
Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
      165      170

```

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 170 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```

Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro

```

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(2) INFORMATION FOR SEO ID NO:42:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEO ID NO:42:

(2) INFORMATION FOR SEO ID NO:43:

(A) LENGTH: 170 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

| | | | | | | | | | | | | | | | |
|----------|-----------|-----------|-----------|----------|-----|-----------|-----------|-----------|-----------|-----|-----------|-----------|-----------|-----|-----|
| Lys 1 | Glu | Ala | Ile | Ser 5 | Pro | Pro | Asp | Ala | Ala 10 | Ser | Ala | Ala | Pro | Leu | Arg |
| Thr | Ile | Thr | Ala 20 | Asp | Thr | Phe | Arg | Lys 25 | Leu | Phe | Arg | Val | Tyr 30 | Ser | Asn |
| Phe | Leu | Arg 35 | Gly | Lys | Leu | Lys | Leu 40 | Tyr | Thr | Gly | Glu | Ala 45 | Cys | Arg | Thr |
| Gly | Asp 50 | Arg | Gly | Gly | Gly | Ser 55 | Ala | Pro | Pro | Arg | Leu 60 | Ile | Cys | Asp | Ser |

```

Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
65      70      75      80
Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
      85      90      95
Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
      100      105      110
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
      115      120      125
Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu
      130      135      140
Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
145      150      155      160
Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln
      165      170

```

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```

Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr
1      5      10      15
Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe
      20      25      30
Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly
      35      40      45
Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg
50      55      60
Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr
65      70      75      80
Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro
      85      90      95
Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln
      100      105      110
Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val
      115      120      125
Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro
      130      135      140
Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr
145      150      155      160
Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys
      165      170

```

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

```

Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile
1      5      10      15
Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu
      20      25      30
Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp
      35      40      45
Arg Gly Gly Gly Ser Ala Pro Arg Leu Ile Cys Asp Ser Arg Val
50      55      60
Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr
65      70      75      80
Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp
      85      90      95
Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln
      100      105      110
Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu

```

```

      115              120              125
Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu
   130              135              140
Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr
   145              150              155
Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
               165              170

```

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

```

Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr
 1      5      10      15
Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg
   20      25      30
Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg
   35      40      45
Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu
   50      55      60
Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly
   65      70      75      80
Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr
   85      90      95
Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala
   100     105     110
Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg
   115     120     125
Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln
   130     135     140
Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu
   145     150     155     160
Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala
               165              170

```

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

```

Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala
 1      5      10      15
Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly
   20      25      30
Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly
   35      40      45
Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu
   50      55      60
Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys
   65      70      75      80
Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys
   85      90      95
Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val
   100     105     110
Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly
   115     120     125
Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu
   130     135     140
His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu
   145     150     155     160
Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile
               165              170

```

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

```

Pro  Pro  Asp  Ala  Ala  Ser  Ala  Ala  Pro  Leu  Arg  Thr  Ile  Thr  Ala  Asp
 1      5      10      15
Thr  Phe  Arg  Lys  Leu  Phe  Arg  Val  Tyr  Ser  Asn  Phe  Leu  Arg  Gly  Lys
 20     25     30
Leu  Lys  Leu  Tyr  Thr  Gly  Glu  Ala  Cys  Arg  Thr  Gly  Asp  Arg  Gly  Gly
 35     40     45
Gly  Ser  Ala  Pro  Pro  Arg  Leu  Ile  Cys  Asp  Ser  Arg  Val  Leu  Glu  Arg
 50     55     60
Tyr  Leu  Leu  Glu  Ala  Lys  Glu  Ala  Glu  Asn  Ile  Thr  Thr  Gly  Cys  Ala
 65     70     75
Glu  His  Cys  Ser  Leu  Asn  Glu  Asn  Ile  Thr  Val  Pro  Asp  Thr  Lys  Val
 85     90     95
Asn  Phe  Tyr  Ala  Trp  Lys  Arg  Met  Glu  Val  Gly  Gln  Gln  Ala  Val  Glu
100    105    110
Val  Trp  Gln  Gly  Leu  Ala  Leu  Leu  Ser  Glu  Ala  Val  Leu  Arg  Gly  Gln
115    120    125
Ala  Leu  Leu  Val  Asn  Ser  Ser  Gln  Pro  Trp  Glu  Pro  Leu  Gln  Leu  His
130    135    140
Val  Asp  Lys  Ala  Val  Ser  Gly  Leu  Arg  Ser  Leu  Thr  Thr  Leu  Leu  Arg
145    150    155    160
Ala  Leu  Gly  Ala  Gln  Lys  Glu  Ala  Ile  Ser
165    170

```

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

```

Pro  Asp  Ala  Ala  Ser  Ala  Ala  Pro  Leu  Arg  Thr  Ile  Thr  Ala  Asp  Thr
 1      5      10      15
Phe  Arg  Lys  Leu  Phe  Arg  Val  Tyr  Ser  Asn  Phe  Leu  Arg  Gly  Lys  Leu
 20     25     30
Lys  Leu  Tyr  Thr  Gly  Glu  Ala  Cys  Arg  Thr  Gly  Asp  Arg  Gly  Gly  Gly
 35     40     45
Ser  Ala  Pro  Pro  Arg  Leu  Ile  Cys  Asp  Ser  Arg  Val  Leu  Glu  Arg  Tyr
 50     55     60
Leu  Leu  Glu  Ala  Lys  Glu  Ala  Glu  Asn  Ile  Thr  Thr  Gly  Cys  Ala  Glu
 65     70     75
His  Cys  Ser  Leu  Asn  Glu  Asn  Ile  Thr  Val  Pro  Asp  Thr  Lys  Val  Asn
 85     90     95
Phe  Tyr  Ala  Trp  Lys  Arg  Met  Glu  Val  Gly  Gln  Gln  Ala  Val  Glu  Val
100    105    110
Trp  Gln  Gly  Leu  Ala  Leu  Leu  Ser  Glu  Ala  Val  Leu  Arg  Gly  Gln  Ala
115    120    125
Leu  Leu  Val  Asn  Ser  Ser  Gln  Pro  Trp  Glu  Pro  Leu  Gln  Leu  His  Val
130    135    140
Asp  Lys  Ala  Val  Ser  Gly  Leu  Arg  Ser  Leu  Thr  Thr  Leu  Leu  Arg  Ala
145    150    155    160
Leu  Gly  Ala  Gln  Lys  Glu  Ala  Ile  Ser  Pro
165    170

```

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

```

Asp Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe
 1      5      10      15
Arg Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys
 20      25      30
Leu Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser
 35      40      45
Ala Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu
 50      55      60
Leu Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His
 65      70      75      80
Cys Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe
 85      90      95
Tyr Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp
100      105      110
Gln Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu
115      120      125
Leu Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp
130      135      140
Lys Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu
145      150      155      160
Gly Ala Gln Lys Glu Ala Ile Ser Pro Pro
165      170

```

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

```

Ala Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg
 1      5      10      15
Lys Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu
 20      25      30
Tyr Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala
 35      40      45
Pro Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu
 50      55      60
Glu Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys
 65      70      75      80
Ser Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr
 85      90      95
Ala Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln
100      105      110
Gly Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu
115      120      125
Val Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys
130      135      140
Ala Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
145      150      155      160
Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp
165      170

```

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

```

Ala Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys

```



```

1      5      10      15
Leu Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr
20      25      30
Thr Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro
35      40      45
Pro Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu
50      55      60
Ala Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser
65      70      75      80
Leu Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala
85      90      95
Trp Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly
100      105      110
Leu Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val
115      120      125
Asn Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
130      135      140
Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala
145      150      155      160
Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala
165      170

```

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

```

Ser Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu
1      5      10      15
Phe Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr
20      25      30
Gly Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro
35      40      45
Arg Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala
50      55      60
Lys Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu
65      70      75      80
Asn Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp
85      90      95
Lys Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu
100      105      110
Ala Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn
115      120      125
Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val
130      135      140
Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln
145      150      155      160
Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala
165      170

```

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

```

Ala Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe
1      5      10      15
Arg Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly
20      25      30
Glu Ala Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg
35      40      45
Leu Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys
50      55      60

```

20250419 10219

Glu Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn
 65 70 75 80
 Glu Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys
 85 90 95
 Arg Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
 100 105 110
 Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser
 115 120 125
 Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser
 130 135 140
 Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys
 145 150 155 160
 Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser
 165 170

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg
 1 5 10 15
 Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu
 20 25 30
 Ala Cys Arg Thr Gly Asp Arg Gly Gly Ser Ala Pro Arg Leu
 35 40 45
 Ile Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu
 50 55 60
 Ala Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu
 65 70 75 80
 Asn Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
 85 90 95
 Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu
 100 105 110
 Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser
 115 120 125
 Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly
 130 135 140
 Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu
 145 150 155 160
 Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala
 165 170

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val
 1 5 10 15
 Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala
 20 25 30
 Cys Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile
 35 40 45
 Cys Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala
 50 55 60
 Glu Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
 65 70 75 80
 Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met
 85 90 95
 Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu
 100 105 110
 Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln

005454 "10219"

```

      115      120      125
Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu
  130      135      140
Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala
  145      150      155      160
Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
      165      170

```

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 171 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```

Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr
 1      5      10      15
Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys
 20      25      30
Arg Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys
 35      40      45
Asp Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
 50      55      60
Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile
 65      70      75      80
Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu
 85      90      95
Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser
 100      105      110
Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro
 115      120      125
Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg
 130      135      140
Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Ala Lys Glu Ala
 145      150      155      160
Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala Pro
      165      170

```

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser
 1      5      10      15
Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg
 20      25      30
Thr Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp
 35      40      45
Ser Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn
 50      55      60
Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr
 65      70      75      80
Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val
 85      90      95
Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Ser Glu
 100      105      110
Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp
 115      120      125
Glu Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser
 130      135      140
Leu Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser
 145      150      155      160
Pro Pro Asp Ala Ala Ser Ala Ala Pro Leu
      165      170

```

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg Val Tyr Ser Asn
 1           5           10           15
Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly Glu Ala Cys Arg Thr
      20           25           30
Gly Asp Arg Gly Gly Gly Ser Ala Pro Pro Arg Leu Ile Cys Asp Ser
      35           40           45
Arg Val Leu Glu Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu Asn Ile
      50           55           60
Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn Ile Thr Val
      65           70           75
Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg Met Glu Val Gly
      85           90           95
Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala Leu Leu Ser Glu Ala
      100          105          110
Val Leu Arg Gly Gln Ala Leu Leu Val Asn Ser Ser Gln Pro Trp Glu
      115          120          125
Pro Leu Gln Leu His Val Asp Lys Ala Val Ser Gly Leu Arg Ser Leu
      130          135          140
Thr Thr Leu Leu Arg Ala Leu Gly Ala Gln Lys Glu Ala Ile Ser Pro
      145          150          155
Pro Asp Ala Ala Ser Ala Ala Pro Leu Arg
      165          170

```

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```

AATATCACGA CGGGCTGTGC TGAACACTGC AGCTTGAATG AGAATATCAC TGTCCCAGAC      60
ACCAAAGTTA ATTTCTATGC CTGGAAGAGG ATGGAGGTCG GGCAGCAGGC CGTAGAAGTC      120
TGGCAGGGCC TGGCCCTGCT GTCGGAAGCT GTCCTGCGGG GCCAGGCCCT GTTGGTCAAC      180
TCTTCCACGC CGTGGGAGCC CCTGCAGCTG CATGTGGATA AAGCCGTCAG TGGCCTTCGC      240
AGCCTCACCA CTCTGCTTCG GGCTCTGGGA GCCCAGAAGG AAGCCATCTC CCCTCCAGAT      300
GCGGCTCCAG CTGCTCCACT CCGAACAATC ACTGCTGACA CTTTCCGCAA ACTCTCCGA      360
GTCTACTCCA ATTTCTCCG GGGAAAGCTG AAGCTGTACA CAGGGGAGGC CTGCAGGACA      420
GGGGACAGAT GAGGCGGCGG CTCCCCCAC CACGCCTCAT CTGTGACAGC CGAGTCTCTG      480
AGAGGTACCT CTTGGAGGCC AAGGAGGCCG AG

```

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```

ATCACGACGG GCTGTGCTGA ACACTGCAGC TTGAATGAGA ATATCACTGT CCCAGACACC      60
AAAGTTAATT TCTATGCCTG GAAGAGGATG GAGGTCGGGC AGCAGGCCGT AGAAGTCTGG      120
CAGGGCCTGG CCCTGCTGTC GGAAGCTGTC CTGCGGGGCC AGGCCCTGTT GGTCAACTCT      180
TCCCAGCCGT GGGAGCCCCT GCAGCTGCAT GTGGATAAAG CCGTCAGTGG CCTTCGCAGC      240
CTCACCCTC TGCTTCGGGC TCTGGGAGCC CAGAAGGAAG CCATCTCCCC TCCAGATGCG      300
GCCTCAGCTG CTCCACTCCG AACAATCACT GCTGACACTT TCCGCAAACCT CTTCCGAGTC      360
TACTCCAATT TCCTCCGGGG AAAGCTGAAG CTGTACACAG GGGAGGCCTG CAGGACAGGG      420
GACAGATGAG CCGGCGGCTC CCCCACCAC GCCTCATCTG TGACAGCCGA GTCCCTGGAGA      480
GGTACCTCTT GGAGGCCAAG GAGGCCGAGA AT

```

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```

ACGACGGGGCT GTGCTGAACA CTGCAGCTTG AATGAGAATA TCACTGTCCC AGACACCAAA      60
GTTAATTTCT ATGCGTGGAA GAGGATGGAG GTCGGGCAGC AGGCCGTAGA AGTCTGGCAG      120
GGCCTGGCCC TGCTGTCGGA AGCTGTCTTG CGGGGCCAGG CCCTGTTGGT CAACTCTTCC      180
CAGCCGTGGG AGCCCCTGCA GCTGCATGTG GATAAAGCCG TCAGTGGCCT TCGCAGCCTC      240
ACCACTCTGC TTCGGGCTCT GGGAGCCCAG AAGGAAGCCA TCTCCCCTCC AGATGCGGCC      300
TCAGCTGCTC CACTCCGAAC AATCACTGCT GACACTTTCC GCAAACCTCT CCGAGTCTAC      360
TCCAATTTCC TCCGGGGAAA GCTGAAGCTG TACACAGGGG AGGCCTGCAG GACAGGGGAC      420
AGATGAGGCG GCGGCTCCCC CCACCAGCC TCATCTGTGA CAGCCGAGTC CTGGAGAGGT      480
ACCTCTTGGA GGCCAAGGAG GCCGAGAATA TC                                     512

```

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```

ACGGGCTGTG CTGAACACTG CAGCTTGAAT GAGAATATCA CTGTCCCAGA CACCAAAGTT      60
AATTCTATG CCTGGAAGAG GATGGAGGTC GGGCAGCAGG CCGTAGAAGT CTGGCAGGGC      120
CTGGCCCTGC TGTCGGAAGC TGTCTGCGG GGCCAGGCCG TGTTGGTCAA CTCTTCCCAG      180
CCGTGGGAGC CCCTGCAGCT GCATGTGGAT AAAGCCGTCA GTGGCCTTCG CAGCCTCACC      240
ACTCTGCTTC GGGCTCTGGG AGCCCAGAAG GAAGCCATCT CCCCTCCAGA TGGCGCCTCA      300
GCTGCTCCAC TCCGAACAAT CACTGCTGAC ACTTTCCGCA AACTCTTCCG AGTCTACTCC      360
AATTTCCTCC GGGGAAAGCT GAAGCTGTAC ACAGGGGAGG CCTGCAGGAC AGGGGACAGA      420
TGAGGCGGCG GCTCCCCCA CCACGCCTCA TCTGTGACAG CCGAGTCCTG GAGAGGTACC      480
TCTTGAGGCG CAAGGAGGCC GAGAATATCA CG                                     512

```

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```

GGCTGTGCTG AACACTGCAG CTTGAATGAG AATATCACTG TCCCAGACAC CAAAGTTAAT      60
TTCTATGCCT GGAAGAGGAT GGAGGTCGGG CAGCAGGCCG TAGAAGTCTG GCAGGCGCTG      120
GCCCTGCTGT CGGAAGCTGT CCTGCGGGGC CAGGCCCTGT TGGTCAACTC TTCCCAGCCG      180
TGGGAGCCCC TGCAGCTGCA TGTGGATAAA GCCGTCAGTG GCCTTCGCAG CCTCACCCT      240
CTGCTTCGGG CTCTGGGAGC CCAGAAGGAA GCCATCTCCC CTCCAGATGC GGCCTCAGCT      300
GCTCCACTCC GAACAATCAC TGCTGACACT TTCCGCAAAC TCTTCCGAGT CTACTCCAAT      360
TTCTCCGGG GAAAGCTGAA GCTGTACACA GGGGAGGCCCT GCAGGACAGG GGACAGATGA      420
GGCGGCGGCT CCCCCACCA CGCCTCATCT GTGACAGCCG AGTCCTGGAG AGGTACCTCT      480
TGGAGGCCAA GGAGGCCGAG AATATCACGA CG                                     512

```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

TGTGCTGAAC ACTGCAGCTT GAATGAGAAT ATCACTGTCC CAGACACCAA AGTTAATTTCT      60
TATGCTTGGA AGAGGATGGA GGTGCGGCAG CAGGCCGTAG AAGTCTGGCA GGGCCTGGCC      120

```

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| CTGCTGTCCG | AAGCTGTCCT | GCGGGGCCAG | GCCCTGTTGG | TCAACTCTTC | CCAGCCGTGG | 180 |
| GAGCCCCTGC | AGCTGCATGT | GGATAAAGCC | GTCAGTGGCC | TTCGCAGCCT | CACCACTCTG | 240 |
| CTTCGGGCTC | TGGGAGCCCA | GAAGGAAGCC | ATCTCCCCCTC | CAGATGCGGC | CTCAGCTGCT | 300 |
| CCACTCCGAA | CAATCACTGC | TGACACTTTC | CGCAAACCTCT | TCCGAGTCTA | CTCCAATTTT | 360 |
| CTCCGGGGAA | AGCTGAAGCT | GTACACAGGG | GAGGCCTGCA | GGACAGGGGA | CAGATGAGGC | 420 |
| GGCGGCTCCC | CCCACCACGC | CTCATCTGTG | ACAGCCGAGT | CCTGGAGAGG | TACCTCTTGG | 480 |
| AGGCCAAGGA | GGCCGAGAAT | ATCACGACGG | GC | | | 512 |

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GCTGAACACT | GCAGCTTGAA | TGAGAATATC | ACTGTCCCAG | ACACCAAAGT | TAATTTCTAT | 60 |
| GCCTGGAAGA | GGATGGAGGT | CGGGCAGCAG | GCCGTAGAAG | TCTGGCAGGG | CCTGGCCCTG | 120 |
| CTGTCGGAAG | CTGTCTTGGC | GGGCCAGGCC | CTGTTGGTCA | ACTCTTCCCA | GCCGTGGGAG | 180 |
| CCCCTGCAAG | TGCATGTGGA | TAAAGCCGTC | AGTGGCCTTC | GCAGCCTCAC | CACTCTGCTT | 240 |
| CGGGCTCTGG | GAGCCAGAA | GGAAGCCATC | TCCCCTCCAG | ATGCGGCCTC | AGCTGCTCCA | 300 |
| CTCCGAACAA | TCACTGCTGA | CACCTTCCGC | AAACTCTTCC | GAGTCTACTC | CAATTTCCCTC | 360 |
| CGGGGAAGAA | TGAAGCTGTA | CACAGGGGAG | GCCTGCAGGA | CAGGGGACAG | ATGAGGCGGC | 420 |
| GGCTCCCCCC | ACCACGCCTC | ATCTGTGACA | GCCGAGTCCT | GGAGAGGTAC | CTCTTGGAGG | 480 |
| CCAAGGAGGC | CGAGAATATC | ACGACGGGCT | GT | | | 512 |

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAACACTGCA | GCTTGAATGA | GAATATCACT | GTCCCAGACA | CCAAAGTTAA | TTTCTATGCC | 60 |
| TGGAAGAGGA | TGGAGGTCGG | GCAGCAGGCC | GTAGAAGTCT | GGCAGGGCCT | GGCCCTGCTG | 120 |
| TCGGAAGCTG | TCCTGCGGGG | CCAGGCCCTG | TTGGTCAACT | CTTCCCAGCC | GTGGGAGCCC | 180 |
| CTGCAGCTGC | ATGTGGATAA | AGCCGTCAGT | GGCCTTCGCA | GCCTCACCAC | TCTGCTTCGG | 240 |
| GCTCTGGGAG | CCCAGAAGGA | AGCCATCTCC | CCTCCAGATG | CGGCCTCAGC | TGCTCCACTC | 300 |
| CGAACAATCA | CTGCTGACAC | TTTCCGCAAA | CTCTTCCGAG | TCTACTCCAA | TTTCCTCCGG | 360 |
| GGAAAGCTGA | AGCTGTACAC | AGGGGAGGCC | TGCAGGACAG | GGGACAGATG | AGGCGGCGGC | 420 |
| TCCCCCACC | ACGCCTCATC | TGTGACAGCC | GAGTCCTGGA | GAGGTACCTC | TTGGAGGCCA | 480 |
| AGGAGGCCGA | GAATATCACG | ACGGGCTGTG | CT | | | 512 |

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CACTGCAGCT | TGAATGAGAA | TATCACTGTC | CCAGACACCA | AAGTTAATTT | CTATGCCTGG | 60 |
| AAGAGGATGG | AGGTCGGGCA | GCAGGCCGTA | GAAGTCTGGC | AGGGCCTGGC | CCTGTCTGTCG | 120 |
| GAAGCTGTCC | TGCGGGGCCA | GGCCCTGTTG | GTCAACTCTT | CCCAGCCGTG | GGAGCCCTCT | 180 |
| CAGTGCATG | TGGATAAAGC | CGTCAGTGCC | CTTCGCAGCC | TCACCACTCT | GCTTCGGGCT | 240 |
| CTGGGAGCCC | AGAAGGAAGC | CATCTCCCTT | CCAGATGCGG | CCTCAGCTGC | TCCACTCCGA | 300 |
| ACAATCACTG | CTGACACTTT | CCGCAAATCT | TTCCGAGTCT | ACTCCAATTT | CCTCCGGGGA | 360 |
| AAGCTGAAGC | TGTACACAGG | GGAGGCCCTG | AGGACAGGGG | ACAGATGAGG | CGGCGGCTCC | 420 |
| CCCCACCACG | CCTCATCTGT | GACAGCCGAG | TCCTGGAGAG | GTACCTCTTG | GAGGCCAAGG | 480 |
| AGGCCGAGAA | TATCACGACG | GGCTGTGCTG | AA | | | 512 |

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| TGCAGCTTGA | ATGAGAATAT | CACTGTCCCA | GACACCAAAG | TTAATTTCTA | TGCCTGGAAG | 60 |
| AGGATGGAGG | TCGGGCAGCA | GGCCGTAGAA | GTCTGGCAGG | GCCTGGCCCT | GCTGTCGGAA | 120 |
| GCTGTCCCTG | GGGGCCAGGC | CCTGTTGGTC | AACTCTTCCC | AGCCGTGGGA | GCCCCGTCAG | 180 |
| CTGCATGTGG | ATAAAGCCGT | CAGTGGCCTT | CGCAGCCTCA | CCACTCTGCT | TCGGGCTCTG | 240 |
| GGAGCCGAGA | AGGAAGCCAT | CTCCCCCTCA | GATGCGGCCCT | CAGCTGCTCC | ACTCCGAACA | 300 |
| ATCACTGCTG | ACACTTTCCG | CAAACCTCTT | CGAGTCTACT | CCAATTTCTT | CCGGGGAAAG | 360 |
| CTGAAGCTGT | ACACAGGGGA | GGCCTGCAGG | ACAGGGGACA | GATGAGGCGG | CGGCTCCCCC | 420 |
| CACCACGCCT | CATCTGTGAC | AGCCGAGTCC | TGGAGAGGTA | CCTCTTGGAG | GCCAAGGAGG | 480 |
| CCGAGAATAT | CACGACGGC | TGTGCTGAAC | AC | | | 512 |

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| AGCTTGAATG | AGAATATCAC | TGTCCCAGAC | ACCAAAGTTA | ATTCTATGCT | CTGGAAGAGG | 60 |
| ATGGAGGTCG | GGCAGCAGGC | CGTAGAAGTC | TGGCAGGGCC | TGGCCCTGCT | GTCCGAAGCT | 120 |
| GTCTGCGGGG | GCCAGGCCCT | GTTGGTCAAC | TCTTCCCAGC | CGTGGGAGCC | CCTGCAGCTG | 180 |
| CATGTGGATA | AAGCCGTCAG | TGGCCTTCGC | AGCCTCACCA | CTCTGCTTCG | GGCTCTGGGA | 240 |
| GCCGAGAAGG | AAGCCATCTC | CCCTCCAGAT | GCGGCCTCAG | CTGCTCCACT | CCGAACAATC | 300 |
| ACTGCTGACA | CTTTCGCAA | ACTCTTCCGA | GTCTACTCCA | ATTTCTCCG | GGGAAAGCTG | 360 |
| AAGCTGTACA | CAGGGGAGGC | CTGCAGGACA | GGGGACAGAT | GAGGCGGCGG | CTCCCCCAC | 420 |
| CACGCCTCAT | CTGTGACAGC | CGAGTCCTGG | AGAGGTACCT | CTTGGAGGCC | AAGGAGGCCG | 480 |
| AGAAATATCAC | GACGGGCTGT | GCTGAACACT | GC | | | 512 |

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTGAATGAGA | ATATCACTGT | CCCAGACACC | AAAGTTAATT | TCTATGCCTG | GAAGAGGATG | 60 |
| GAGGTCCGGC | AGCAGGCCGT | AGAAGTCTGG | CAGGGCCTGG | CCCTGCTGTC | GGAAGCTGTC | 120 |
| CTGCGGGGCC | AGGCCCTGTT | GGTCAACTCT | TCCCAGCCGT | GGGAGCCCTT | GCAGCTGCAT | 180 |
| GTGGATAAAG | CCGTCACTGG | CCTTCGCAGC | CTCACCACCT | TGCTTCGGGC | TCTGGGAGCC | 240 |
| CAGAAGGAAG | CCATCTCCCC | TCCAGATGCG | GCCTCAGCTG | CTCCACTCCG | AACAATCACT | 300 |
| GCTGACACTT | TCCGCAAACT | CTTCCGAGTC | TACTCCAATT | TCCTCCGGGG | AAAGCTGAAG | 360 |
| CTGTACACAG | GGGAGGCCTG | CAGGACAGGG | GACAGATGAG | GCGGCGGCTC | CCCCACCAC | 420 |
| GCCTCATCTG | TGACAGCCGA | GTCTTGGAGA | GGTACCTCTT | GGAGGCCAAG | GAGGCCGAGA | 480 |
| ATATCACGAC | GGGCTGTGCT | GAACACTGCA | GC | | | 512 |

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| AATGAGAATA | TCACTGTCCC | AGACACCAAA | GTTAATTTCT | ATGCCTGGAA | GAGGATGGAG | 60 |
| GTCCGGCAGC | AGGCCGTAGA | AGTCTGGCAG | GGCCTGGCCC | TGCTGTGCGA | AGCTGTCTCT | 120 |
| CGGGGCCAGG | CCCTGTTGGT | CAACTCTTCC | CAGCCGTGGG | AGCCCTTGCA | GCTGCATGTG | 180 |
| GATAAAGCCG | TCAGTGGCCT | TGCGAGCCTC | ACCACTCTGC | TTCCGGGCTCT | GGGAGCCGAG | 240 |
| AAGGAAGCCA | TCTCCCTTCC | AGATGCGGCC | TCAGCTGCTC | CACTCCGAAC | AATCACTGCT | 300 |
| GACACTTTCC | GCAAACCTCT | CCGAGTCTAC | TCCAATTTCC | TCCGGGGAAA | GCTGAAGCTG | 360 |
| TACACAGGGG | AGGCCGTGAG | GACAGGGGAC | AGATGAGGCG | GCGGCTCCCC | CCACCAGGCC | 420 |
| TCATCTGTGA | CAGCCGAGTC | CTGGAGAGGT | ACCTCTTGGA | GGCCAAGGAG | GCCGAGAATA | 480 |
| TCACGACGGG | CTGTGCTGAA | CACTGCAGCT | TG | | | 512 |

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|-----|
| GAGAATATCA | CTGTCCCAGA | CACCAAAGTT | AATTTCTATG | CCTGGAAGAG | GATGGAGGTC | 60 |
| GGGCAGCAGG | CCGTAGAAGT | CTGGCAGGGC | CTGGCCCTGC | TGTCGGAAGC | TGTCCCTGCGG | 120 |
| GGCCAGGCCC | TGTTGGTCAA | CTCTTCCCAG | CCGTGGGAGC | CCCTGCAGCT | GCATGTGGAT | 180 |
| AAAGCCGTCA | GTGGCCTTCG | CAGCCTCACC | ACTCTGCTTC | GGGCTCTGGG | AGCCCAGAAG | 240 |
| GAAGCCATCT | CCCCCTCCAG | TGCGGCCCTCA | GCTGCTCCAC | TCCGAACAAT | CACTGCTGAC | 300 |
| ACTTTCCGCA | AACTCTTCCG | AGTCTACTCC | AATTTCTCTC | GGGGAAAGCT | GAAGCTGTAC | 360 |
| ACAGGGGAGG | CCTGCAGGAC | AGGGGACAGA | TGAGGCGGCG | GCTCCCCCCA | CCACGCCTCA | 420 |
| TCTGTGACAG | CCGAGTCCTG | GAGAGGTACC | TCTTGGAGGC | CAAGGAGGCC | GAGAATATCA | 480 |
| CGACGGGCTG | TGCTGAACAC | TGCAGCTTGA | AT | | | 512 |

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| AATATCACTG | TCCCAGACAC | CAAAGTTAAT | TTCTATGCCT | GGAAGAGGAT | GGAGGTCGGG | 60 |
| CAGCAGGCCG | TAGAAGTCTG | GCAGGGCCTG | GCCCTGCTGT | CGGAAGCTGT | CCTGCGGGGGC | 120 |
| CAGGCCCTGT | TGGTCAACTC | TTCCCAGCCG | TGGGAGCCCC | TGCAGCTGCA | TGTGGATAAAA | 180 |
| GCCGTCACTG | GCCTTCGCAG | CCTCACCCT | CTGCTTCGGG | CTCTGGGAGC | CCAGAAGGAA | 240 |
| GCCATCTCCC | CTCCAGATGC | GGCCTCAGCT | GCTCCACTCC | GAACAATCAC | TGCTGACACT | 300 |
| TTCCGCAAAAC | TCTTCCGAGT | CTACTCCAAT | TTCTCCCGGG | GAAAGCTGAA | GCTGTACACA | 360 |
| GGGGAGGCCT | GCAGGACAGG | GGACAGATGA | GGCGGCGGCT | CCCCCACCA | CGCCTCATCT | 420 |
| GTGACAGCCG | AGTCCTGGAG | AGGTACCTCT | TGGAGGCCAA | GGAGGCCGAG | AATATCACGA | 480 |
| CGGGCTGTGC | TGAACACTGC | AGCTTGAATG | AG | | | 512 |

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| ATCACTGTCC | CAGACACCAA | AGTTAATTTT | TATGCCTGGA | AGAGGATGGA | GGTCGGGCAG | 60 |
| CAGGCCGTAG | AAGTCTGGCA | GGGCCTGGCC | CTGCTGTCCG | AAGCTGTCCT | GCGGGGCCAG | 120 |
| GCCCTGTTGG | TCAACTCTTC | CCAGCCGTGG | GAGCCCCTGC | AGCTGCATGT | GGATAAAGCC | 180 |
| GTCAGTGGCC | TTTCGCAGCT | CACCACTCTG | CTTCGGGCTC | TGGGAGCCCA | GAAGGAAGCC | 240 |
| ATCTCCCCCT | CAGATGCGGC | CTCAGCTGCT | CCACTCCGAA | CAATCACTGC | TGACACTTTC | 300 |
| CGCAAACCTCT | TCCGAGTCTA | CTCCAATTTT | CTCCGGGGAA | AGCTGAAGCT | GTACACAGGG | 360 |
| GAGGCCTGCA | GGACAGGGGA | CAGATGAGGC | GGCGGCTCCC | CCCACCACGC | CTCATCTGTG | 420 |
| ACAGCCGAGT | CCTGGAGAGG | TACCTCTTGG | AGGCCAAGGA | GGCCGAGAAT | ATCACGACGG | 480 |
| GCTGTGCTGA | ACACTGCAGC | TTGAATGAGA | AT | | | 512 |

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACTGTCCCAG | ACACCAAAGT | TAATTTCTAT | GCCTGGAAGA | GGATGGAGGT | CGGGCAGCAG | 60 |
| GGCGTAGAAG | TCTGGCAGGG | CCTGGCCCTG | CTGTGGAAG | CTGTCCTGCG | GGGCCAGGCC | 120 |

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| CTGTTGGTCA | ACTCTTCCCA | GCCGTGGGAG | CCCCTGCAGC | TGCATGTGGA | TAAAGCCGTC | 180 |
| AGTGGCCTTC | GCAGCCTCAC | CACTCTGCTT | CGGGCTCTGG | GAGCCCAGAA | GGAGCCATC | 240 |
| TCCCCTCCAG | ATGCGGCCTC | AGCTGCTCCA | CTCCGAACAA | TCACTGCTGA | CACCTTCCGC | 300 |
| AAACTCTTCC | GAGTCTACTC | CAATTTCCCTC | CGGGGAAAGC | TGAAGCTGTA | CACAGGGGAG | 360 |
| GCCTGCAGGA | CAGGGGACAG | ATGAGGCGGC | GGCTCCCCCC | ACCACGCCTC | ATCTGTGACA | 420 |
| GCCGAGTCCT | GGAGAGGTAC | CTCTTGGAGG | CCAAGGAGGC | CGAGAATATC | ACGACGGGCT | 480 |
| GTCTGAACA | CTGCAGCTTG | AATGAGAATA | ATC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCCCAGACA | CCAAAGTTAA | TTTCTATGCC | TGGAAGAGGA | TGGAGGTCGG | GCAGCAGGCC | 60 |
| GTAGAAGTCT | GGCAGGGCCT | GGCCCTGCTG | TCGGAAGCTG | TCCTGCGGGG | CCAGGCCCTG | 120 |
| TTGGTCAACT | CTTCCAGGCC | GTGGGAGGCC | CTGCAGCTGC | ATGTGGATAA | AGCCGTCAGT | 180 |
| GGCCTTCGCA | GCCTCACCAC | TCTGCTTCGG | GCTCTGGGAG | CCCAGAAGGA | AGCCATCTCC | 240 |
| CCTCCAGATG | CGGCCTCAGC | TGCTCCACTC | CGAACAATCA | CTGCTGACAC | TTTCCGCAAA | 300 |
| CTCTTCCGAG | TCTACTCCAA | TTTCTCCCGG | GGAAAGCTGA | AGCTGTACAC | AGGGGAGGCC | 360 |
| TGCAGGACAG | GGGACAGATG | AGGCGGCGGC | TCCCCCACC | ACGCCTCATC | TGTGACAGCC | 420 |
| GAGTCCTGGA | GAGGTACCTC | TTGGAGGCCA | AGGAGGCCGA | GAATATCACG | ACGGGCTGTG | 480 |
| CTGAACACTG | CAGCTTGAAT | GAGAATAATC | ACT | | | 513 |

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

| | | | | | | |
|------------|------------|-------------|------------|------------|-------------|-----|
| CCAGACACCA | AAGTTAATTT | CTATGCCTGG | AAGAGGATGG | AGGTCGGGCA | GCAGGCCGTA | 60 |
| GAAGTCTGGC | AGGGCCTGGC | CCTGCTGTCC | GAAGCTGTCC | TGCGGGGCCA | GGCCCTGTTG | 120 |
| GTCAACTCTT | CCCAGCCGTG | GGAGCCCCCTG | CAGCTGCATG | TGGATAAAGC | CGTCAGTGGC | 180 |
| CTTCGCAGCC | TCACCACTCT | GCTTCGGGCT | CTGGGAGCCC | AGAAGGAAGC | CATCTCCCCCT | 240 |
| CCAGATGCGG | CCTCAGCTGC | TCCACTCCGA | ACAATCACTG | CTGACACTTT | CCGCAAACCTC | 300 |
| TTCCGAGTCT | ACTCCAATTT | CCTCCGGGGA | AAGCTGAAGC | TGTACACAGG | GGAGGCCTGC | 360 |
| AGGACAGGGG | ACAGATGAGG | CGGCGGCTCC | CCCCACCACG | CCTCATCTGT | GACAGCCGAG | 420 |
| TCCTGGAGAG | GTACCTCTTG | GAGGCCAAGG | AGGCCGAGAA | TATCACGACG | GGCTGTGCTG | 480 |
| AACACTGCAG | CTTGAATGAG | AATAATCACT | GTC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

| | | | | | | |
|------------|-------------|------------|-------------|------------|-------------|-----|
| GACACCAAAG | TTAATTTCTA | TGCCTGGAAG | AGGATGGAGG | TCGGGCAGCA | GGCCGTAGAA | 60 |
| GTCTGGCAGG | GCCTGGCCCT | GCTGTGCGAA | GCTGTCTCTG | GGGGCCAGGC | CCTGTTGGTC | 120 |
| AACTCTTCCC | AGCCGTGGGA | GCCCCTGCA | CTGCATGTGG | ATAAAGCCGT | CAGTGGCCTT | 180 |
| CGCAGCCTCA | CACTCTGCTG | TCGGGCTCTG | GGAGCCCAGA | AGGAAGCCAT | CTCCCCCTCCA | 240 |
| GATGCGGCCT | CAGCTGCTCC | ACTCCGAACA | ATCACTGCTG | ACACTTTCCG | CAAACCTCTT | 300 |
| CGAGTCTACT | CCAATTTCCCT | CCGGGGAAAG | CTGAAGCTGT | ACACAGGGGA | GGCCTGCAGG | 360 |
| ACAGGGGACA | GATGAGCGGG | CGGCTCCCCC | CACCACGCCCT | CATCTGTGAC | AGCCGAGTCC | 420 |
| TGGAGAGGTA | CCTCTTGGAG | GCCAAGGAGG | CCGAGAATAT | CACGACGGGC | TGTGCTGAAC | 480 |
| ACTGCAGCTT | GAATGAGAAT | AATCACTGTC | CCA | | | 513 |

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AGGATGGAGG | TCGGGCAGCA | GGCCGTAGAA | GTCTGGCAGG | GCCTGGCCCT | GCTGTCGGAA | 60 |
| GCTGTCTTGC | GGGGCCAGGC | CCTGTTGGTC | AACTCTTCCC | AGCCGTGGGA | GCCCCTGCA | 120 |
| CTGCATGTGG | ATAAAGCCGT | CAGTGGCCTT | CGCAGCCTCA | CCACTCTGCT | TCGGGCTCTG | 180 |
| GGAGCCCAGA | AGGAAGCCAT | CTCCCCTCCA | GATGCGGCCT | CAGCTGCTCC | ACTCCGAACA | 240 |
| ATCACTGCTG | ACACTTTCGG | CAAACCTCTC | CGAGTCTACT | CCAATTTCTT | CCGGGGAAAG | 300 |
| CTGAAGCTGT | ACACAGGGGA | GGCCTGCAGG | ACAGGGGACA | GATGAGGCGG | CGGCTCCCCC | 360 |
| CACCACGCCT | CATCTGTGAC | AGCCGAGTCC | TGGAGAGGTA | CCTCTTGGAG | GCCAAGGAGG | 420 |
| CCGAGAATAT | CACGACGGGC | TGTGCTGAAC | ACTGCAGCTT | GAATGAGAAT | AATCACTGTC | 480 |
| CCAGACACCA | AAGTTAATTT | CTATGCCTGG | AAG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATGGAGGTCG | GGCAGCAGGC | CGTAGAAGTC | TGGCAGGGCC | TGGCCCTGCT | GTCGGAAGCT | 60 |
| GTCTTGC | GCCAGGCCCT | GTTGGTCAAC | TCTTCCCAGC | CGTGGGAGCC | CCTGCAGCTG | 120 |
| CATGTGGATA | AAGCCGTCAG | TGGCCTTCGC | AGCCTCACCA | CTCTGCTTCG | GGCTCTGGGA | 180 |
| GCCCAGAAGG | AAGCCATCTC | CCCTCCAGAT | GCGGCCTCAG | CTGCTCCACT | CCGAACAATC | 240 |
| ACTGCTGACA | CTTTCCGCAA | ACTCTTCCGA | GTCTACTCCA | ATTTCCTCCG | GGGAAAGCTG | 300 |
| AAGCTGTACA | CAGGGGAGGC | CTGCAGGACA | GGGGACAGAT | GAGGCGGCGG | CTCCCCCAC | 360 |
| CACGCCTCAT | CTGTGACAGC | CGAGTCCTGG | AGAGGTACCT | CTTGGAGGCC | AAGGAGGCCG | 420 |
| AGAAATACAC | GACGGGTGTG | GCTGAACACT | GCAGCTTGAA | TGAGAATAAT | CACGTGTCCA | 480 |
| GACACCAAAG | TTAATTCTTA | TGCCTGGAAG | AGG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GAGGTCGGGC | AGCAGGCCGT | AGAAGTCTGG | CAGGGCCTGG | CCCTGCTGTC | GGAAGCTGTC | 60 |
| CTGCGGGGCC | AGGCCCTGTT | GGTCAACTCT | TCCCAGCCGT | GGGAGCCCCT | GCAGCTGCAT | 120 |
| GTGGATAAAG | CCGTCACTGG | CCTTCGCAGC | CTCACCCTCT | TGCTTCGGGC | TCTGGGAGCC | 180 |
| CAGAAGGAAG | CCATCTCCCC | TCCAGATGCG | GCCTCAGCTG | CTCCACTCCG | AACAATCACT | 240 |
| GCTGACACTT | TCCGCAAACT | CTTCCGAGTC | TACTCCAATT | TCCTCCGGGG | AAAGCTGAAG | 300 |
| CTGTACACAG | GGGAGGCCTG | CAGGACAGGG | GACAGATGAG | GCGGCGGCTC | CCCCACCAC | 360 |
| GCCTCATCTG | TGACAGCCGA | GTCCTGGAGA | GGTACCTCTT | GGAGGCCAAG | GAGGCCGAGA | 420 |
| ATATCACGAC | GGGCTGTGCT | GAACACTGCA | GCTTGAATGA | GAATAATCAC | TGTCCCAGAC | 480 |
| ACCAAAGTTA | ATTTCTATGC | CTGGAAGAGG | ATG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GTCGGGCAGC | AGGCCGTAGA | AGTCTGGCAG | GGCCTGGCCC | TGCTGTCGGA | AGCTGTCTCTG | 60 |
| CGGGGCCAGG | CCCTGTGGT | CAACTCTTCC | CAGCCGTGGG | AGCCCTTGCA | GCTGCATGTG | 120 |
| GATAAAGCCG | TCAGTGGCCT | TCGCAGCCTC | ACCACTCTGC | TTCGGGCTCT | GGGAGCCAG | 180 |
| AAGGAAGCCA | TCTCCCTTCC | AGATGCGGCC | TCAGCTGCTC | CACTCCGAAC | AATCACTGCT | 240 |
| GACACTTTCC | GCAAACTCTT | CCGAGTCTAC | TCCAATTTCC | TCCGGGGAAA | GCTGAAGCTG | 300 |
| TACACAGGGG | AGGCCTGCAG | GACAGGGGAC | AGATGAGGCG | GCGGCTCCCC | CCACCACGCC | 360 |
| TCATCTGTGA | CAGCCGAGTC | CTGGAGAGGT | ACCTCTTGGA | GGCCAAGGAG | GCCGAGAATA | 420 |
| TCACGACGGG | CTGTGCTGAA | CACTGCAGCT | TGAATGAGAA | TAATCACTGT | CCCAGACACC | 480 |
| AAAGTTAATT | TCTATGCCTG | GAAGAGGATG | GAG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| CAGGCCCTGT | TGGTCAACTC | TTCCCAGCCG | TGGGAGCCCC | TGCAGCTGCA | TGTGGATAAA | 60 |
| GCCGTCAGTG | GCCTTCGCAG | CCTCACCAC | CTGCTTCGGG | CTCTGGGAGC | CCAGAAGGAA | 120 |
| GCCATCTCCC | CTCCAGATGC | GGCCTCAGCT | GCTCCACTCC | GAACAATCAC | TGCTGACACT | 180 |
| TTCCGCAAAAC | TCTTCCGAGT | CTACTCCAAT | TTCTTCCGGG | GAAAGCTGAA | GCTGTACACA | 240 |
| GGGAGGCCT | GCAGGACAGG | GGACAGATGA | GGCGGCGGCT | CCCCCACCA | CGCCTCATCT | 300 |
| GTGACAGCCG | AGTCCTGGAG | AGGTACCTCT | TGGAGGCCAA | GGAGGCCGAG | AATATCACGA | 360 |
| CGGGCTGTGC | TGAACACTGC | AGCTTGAATG | AGAATAATCA | CTGTCCCAGA | CACCAAAGTT | 420 |
| AATTCTATG | CCTGGAAGAG | GATGGAGGTC | GGGCAGCAGG | CCGTAGAAGT | CTGGCAGGGC | 480 |
| CTGGCCCTGC | TGTCGAAGC | TGTCCTGGCG | GGC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GCCCTGTTGG | TCAACTCTTC | CCAGCCGTGG | GAGCCCCTGC | AGCTGCATGT | GGATAAAGCC | 60 |
| GTCAGTGGCC | TTCGCAGCCT | CACCACTCTG | CTTCGGGCTC | TGGGAGCCCA | GAAGGAAGCC | 120 |
| ATCTCCCCTC | CAGATGCGGC | CTCAGCTGCT | CCACTCCGAA | CAATCACTGC | TGACACTTTC | 180 |
| CGCAAACCTCT | TCCGAGTCTA | CTCCAATTTC | CTCCGGGGAA | AGCTGAAGCT | GTACACAGGG | 240 |
| GAGGCTGCA | GGACAGGGGA | CAGATGAGG | GGCGGCTCCC | CCCACCACGC | CTCATCTGTG | 300 |
| ACAGCCGAGT | CCTGGAGAGG | TACCTCTTGG | AGGCCAAGGA | GGCCGAGAAT | ATCACGACGG | 360 |
| GCTGTGCTGA | AACTGCGAGC | TTGAATGAGA | ATAATCACTG | TCCCAGACAC | CAAAGTTAAT | 420 |
| TTCTATGCCT | GGAAGAGGAT | GGAGGTCGGG | CAGCAGGCCG | TAGAAGTCTG | GCAGGGCCTG | 480 |
| GCCCTGCTGT | CGGAAGCTGT | CCTGCGGGGC | CAG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGTTGGTCA | ACTCTTCCCA | GCCGTGGGAG | CCCCTGCAGC | TGCATGTGGA | TAAAGCCGTC | 60 |
| AGTGGCCTTC | GCAGCCTCAC | CACTCTGCTT | CGGGCTCTGG | GAGCCCAGAA | GGAAGCCATC | 120 |
| TCCCCTCCAG | ATGCGGCCTC | AGCTGCTCCA | CTCCGAACAA | TCACTGTGTA | CACCTTCCGC | 180 |
| AAACTCTTCC | GAGTCTACTC | CAATTTCTCT | CGGGGAAAGC | TGAAGCTGTA | CACAGGGGAG | 240 |
| GCCTGCAGGA | CAGGGGACAG | ATGAGGCGGC | GGCTCCCCC | ACCACGCCTC | ATCTGTGACA | 300 |
| GCCGAGTCCT | GGAGAGGTAC | CTCTTGGAGG | CCAAGGAGGC | CGAGAATATC | ACGACGGGCT | 360 |
| GTGCTGAACA | CTGCAGCTTG | AATGAGAATA | ATCACTGTCC | CAGACACCAA | AGTTAATTTT | 420 |
| TATGCCTGGA | AGAGGATGGA | GGTCGGGCAG | CAGGCCGTAG | AAGTCTGGCA | GGGCCTGGCC | 480 |
| CTGCTGTCCG | AAGCTGTCTC | GCGGGGCCAG | GCC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TTGGTCAACT | CTTCCCAGCC | GTGGGAGCCC | CTGCAGCTGC | ATGTGGATAA | AGCCGTCAGT | 60 |
| GGCCTTCGCA | GCCTCACAC | TCTGCTTCGG | GCTCTGGGAG | CCCAGAAGGA | AGCCATCTCC | 120 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCTCCAGATG | CGGCCTCAGC | TGCTCCACTC | CGAACAATCA | CTGCTGACAC | TTTCCGCAAA | 180 |
| CTCTTCCGAG | TCTACTCCAA | TTTCCTCCGG | GGAAAGCTGA | AGCTGTACAC | AGGGGAGGCC | 240 |
| TGCAGGACAG | GGGACAGATG | AGGCGGCGGC | TCCCCCACC | ACGCCTCATC | TGTGACAGCC | 300 |
| GAGTCTTGGA | GAGGTACCTC | TTGGAGGCCA | AGGAGGCCGA | GAATATCACG | ACGGGCTGTG | 360 |
| CTGAACACTG | CAGCTTGAAT | GAGAATAATC | ACTGTCCCAG | ACACCAAAGT | TAATTTCTAT | 420 |
| GCCTGGAAGA | GGATGGAGGT | CGGGCAGCAG | GCCGTAGAAG | TCTGGCAGGG | CCTGGCCCTG | 480 |
| CTGTCGGAAG | CTGTCTGCG | GGGCCAGGCC | CTG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GTCAACTCTT | CCCAGCCGTG | GGAGCCCCTG | CAGCTGCATG | TGGATAAAGC | CGTCAGTGGC | 60 |
| CTTCGCAGCC | TCACCACTCT | GCTTCGGGCT | CTGGGAGCCC | AGAAGGAAGC | CATCTCCCTT | 120 |
| CCAGATGCGG | CCTCAGCTGC | TCCACTCCGA | ACAATCACTG | CTGACACTTT | CCGCAAATC | 180 |
| TTCCGAGTCT | ACTCCAATTT | CCTCCGGGGA | AAGCTGAAGC | TGTACACAGG | GGAGGCCTGC | 240 |
| AGGACAGGGG | ACAGATGAGG | CGGCGGCTCC | CCCCACCACG | CCTCATCTGT | GACAGCCGAG | 300 |
| TCCTGGAGAG | GTACCTCTTG | GAGGCCAAGG | AGGCCGAGAA | TATCACGACG | GGCTGTGCTG | 360 |
| AACACTGCAG | CTTGAATGAG | AATAATCACT | GTCCCAGACA | CCAAAGTTAA | TTTCTATGCC | 420 |
| TGGAAGAGGA | TGGAGGTCGG | GCAGCAGGCC | GTAAGAAGCT | GGCAGGGCCT | GGCCCTGCTG | 480 |
| TCGGAAGCTG | TCCTGCGGGG | CCAGGCCCTG | TTG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AACTCTTCCC | AGCCGTGGGA | GCCCCTGCAG | CTGCATGTGG | ATAAAGCCGT | CAGTGGCCTT | 60 |
| CGCAGCCTCA | CCACTTGTCT | TCGGGCTCTG | GGAGCCCAGA | AGGAAGCCAT | CTCCCCTCCA | 120 |
| GATGCGGCCT | CAGCTGCTCC | ACTCCGAACA | ATCACTGCTG | ACACTTTCCG | CAAACCTTTC | 180 |
| CGAGTCTACT | CCAATTTCCT | CCGGGGAAAG | CTGAAGCTGT | ACACAGGGGA | GGCCTGCAGG | 240 |
| ACAGGGGACA | GATGAGGCGG | CGGCTCCCCC | CACCACGCCT | CATCTGTGAC | AGCCGAGTCC | 300 |
| TGGAGAGGTA | CCTCTTGGAG | GCCAAGGAGG | CCGAGAATAT | CACGACGGGC | TGTGCTGAAC | 360 |
| ACTGCAGCTT | GAATGAGAAT | AATCACTGTC | CCAGACACCA | AAGTTAATTT | CTATGCCTGG | 420 |
| AAGAGGATGG | AGGTGCGGCA | GCAGGCCGTA | GAAGTCTGGC | AGGGCCTGGC | CCTGCTGTGC | 480 |
| GAAGCTGTCC | TGCGGGGCCA | GGCCCTGTTG | GTC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TCTTCCCAGC | CGTGGGAGCC | CCTGCAGCTG | CATGTGGATA | AAGCCGTCAG | TGGCCTTCGC | 60 |
| AGCCTCACCA | CTCTGCTTCG | GGCTCTGGGA | GCCCAGAAGG | AAGCCATCTC | CCCTCCAGAT | 120 |
| GCGGCCTCAG | CTGCTCCACT | CCGAACAATC | ACTGCTGACA | CTTCCGCAA | ACTCTCCGA | 180 |
| GTCTACTCCA | ATTTCTCCG | GGGAAAGCTG | AAGCTGTACA | CAGGGGAGGC | CTGCAGGACA | 240 |
| GGGACAGAT | GAGGCGCGG | CTCCCCCAC | CACGCCTCAT | CTGTGACAGC | CGAGTCCTGG | 300 |
| AGAGGTACCT | CTTGGAGGCC | AAGGAGGCCG | AGAATATCAC | GACGGGCTGT | GCTGAACACT | 360 |
| GCAGCTTGAA | TGAGAAATAT | CACTGTCCCA | GACACCAAAG | TTAATTTCTA | TGCTGGAAG | 420 |
| AGGATGGAGG | TCGGGCAGCA | GGCCGTAGAA | GTCTGGCAGG | GCCTGGCCCT | GCTGTCGGAA | 480 |
| GCTGTCTTGC | GGGGCCAGGC | CCTGTTGGTC | AAC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| TCCCAGCCGT | GGGAGCCCCT | GCAGCTGCAT | GTGGATAAAG | CCGTCAGTGG | CCTTCGCAGC | 60 |
| CTCACCACCTC | TGCTTCGGGC | TCTGGGAGCC | CAGAAGGAAG | CCATCTCCCC | TCCAGATGCG | 120 |
| GCCTCAGCTG | CTCCACTCCG | AACAATCACT | GCTGACACTT | TCCGCAAAC | CTTCCGAGTC | 180 |
| TACTCCAATT | TCCTCCGGGG | AAAGCTGAAG | CTGTACACAG | GGGAGGCCTG | CAGGACAGGG | 240 |
| GACAGATGAG | GCGGCGGCTC | CCCCACCAC | GCCTCATCTG | TGACAGCCGA | GTCCTGGAGA | 300 |
| GGTACCTCTT | GGAGGCCAAG | GAGGCCGAGA | ATATCACGAC | GGGCTGTGCT | GAACACTGCA | 360 |
| GCTTGAATGA | GAATAATCAC | TGTCCCAGAC | ACCAAAGTTA | ATTTCTATGC | CTGGAAGAGG | 420 |
| ATGGAGGTCG | GGCAGCAGGC | CGTAGAAGTC | TGGCAGGGCC | TGGCCCTGCT | GTCGGAAGCT | 480 |
| GTCTGCGGG | GCCAGGCCCT | GTTGGTCAAC | TCT | | | 513 |

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

| | | | | | | |
|------------|-------------|------------|------------|------------|-------------|-----|
| CAGCCGTGGG | AGCCCCTGCA | GCTGCATGTG | GATAAAGCCG | TCAGTGGCCT | TCGCAGCCTC | 60 |
| ACCACTCTGC | TTCGGGCTCT | GGGAGCCCAG | AAGGAAGCCA | TCTCCCCTCC | AGATGCGGGC | 120 |
| TCAGCTGCTC | CACCTCCGAAC | AATCACTGCT | GACACTTTCC | GCAAACCTCT | CCGAGTCTAC | 180 |
| TCCAATTTCC | TCCGGGAAA | GCTGAAGCTG | TACACAGGGG | AGGCCTGCAG | GACAGGGGAC | 240 |
| AGATGAGGCG | GCGGCTCCCC | CCACCACGCC | TCATCTGTGA | CAGCCGAGTC | CTGGAGAGGT | 300 |
| ACCTCTTGGA | GGCCAAGGAG | GCCGAGAATA | TCACGACGGG | CTGTGCTGAA | CACCTGCAGCT | 360 |
| TGAATGAGAA | TAATCACTGT | CCCAGACACC | AAAGTTAATT | TCTATGCCTG | GAAGAGGATG | 420 |
| GAGGTGCGGC | AGCAGGCCGT | AGAAGTCTGG | CAGGGCCTGG | CCCTGCTGTC | GGAAGCTGTC | 480 |
| CTGCGGGGCC | AGGCCCTGTT | GGTCAACTCT | TCC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCGTGGGAGC | CCCTGCAGCT | GCATGTGGAT | AAAGCCGTCA | GTGGCCTTCG | CAGCCTCACC | 60 |
| ACTCTGCTTC | GGGCTCTGGG | AGCCCAGAAG | GAAGCCATCT | CCCCCAGAGA | TGCGGCCTCA | 120 |
| GCTGCTCCAC | TCCGAACAAT | CACTGCTGAC | ACTTTCCGCA | AACTCTTCCG | AGTCTACTCC | 180 |
| AATTTCCCTC | GGGGAAAGCT | GAAGCTGTAC | ACAGGGGAGG | CCTGCAGGAC | AGGGGACAGA | 240 |
| TGAGGCGGCG | GCTCCCCCA | CCACGCCTCA | TCTGTGACAG | CCGAGTCTCT | GAGAGGTACC | 300 |
| TCTTGGAGGC | CAAGGAGGCC | GAGAATATCA | CGACGGGCTG | TGCTGAACAC | TGCAGCTTGA | 360 |
| ATGAGAATAA | TCAGTGTCCC | AGACACCAA | GTAAATTTCT | ATGCCTGGAA | GAGGATGGAG | 420 |
| GTCGGGCAGC | AGGCCGTAGA | AGTCTGGCAG | GGCCTGGCCC | TGCTGTGCGA | AGCTGTCTCT | 480 |
| CGGGGCCAGG | CCCTGTTGGT | CAACTCTTCC | CAG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| TGGGAGCCCC | TGCAGCTGCA | TGTGGATAAA | GCCGTCAGTG | GCCTTCGCAG | CCTCACCAC | 60 |
| CTGCTTCGGG | CTCTGGGAGC | CCAGAAGGAA | GCCATCTCCC | CTCCAGATGC | GGCCTCAGCT | 120 |
| GCTCCACTCC | GAACAATCAC | TGCTGACACT | TTCCGCAAAC | TCTTCCGAGT | CTACTCCAAT | 180 |
| TTCTTCCGGT | GAAAGCTGAA | GCTGTACACA | GGGGAGGCC | GCAGGACAGG | GGACAGATGA | 240 |
| GGCGGCGGCT | CCCCCAACCA | CGCCTCATCT | GTGACAGCCG | AGTCCTGGAG | AGGTACCTCT | 300 |
| TGGAGGCCAA | GGAGGCCGAG | AATATCACGA | CGGGCTGTGC | TGAACACTGC | AGCTTGAATG | 360 |
| AGAATAATCA | CTGTCCAGAG | CACCAAAGTT | AATTTCTATG | CCTGGAAGAG | GATGGAGGTC | 420 |
| GGCAGCAGG | CCGTAGAAGT | CTGGCAGGGC | CTGGCCCTGC | TGTCGGAAGC | TGCTCTGCGG | 480 |
| GGCCAGGCC | TGTTGGTCAA | CTCTTCCCAG | CCG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|-----|
| GAGCCCCTGC | AGCTGCATGT | GGATAAAGCC | GTCAGTGGCC | TTCGCAGCCT | CACCACTCTG | 60 |
| CTTCGGGGCTC | TGGGAGCCCA | GAAGGAAGCC | ATCTCCCCCTC | CAGATGCGGC | CTCAGCTGCT | 120 |
| CCACTCCGAA | CAATCACTGC | TGACACTTTC | CGCAAACCTCT | TCCGAGTCTA | CTCCAATTTC | 180 |
| CTCCGGGGAA | AGCTGAAGCT | GTACACAGGG | GAGGCCTGCA | GGACAGGGGA | CAGATGAGGC | 240 |
| GGCGGCTCCC | CCCACCACGC | CTCATCTGTG | ACAGCCGAGT | CCTGGAGAGG | TACCTCTTGG | 300 |
| AGGCCAAGGA | GGCCGAGAAT | ATCACGACGG | GCTGTGCTGA | ACACTGCAGC | TTGAATGAGA | 360 |
| ATAATCACTG | TCCCAGACAC | CAAAGTTAAT | TTCTATGCCCT | GGAAGAGGAT | GGAGGTCGGG | 420 |
| CAGCAGGCCG | TAGAAGTCTG | GCAGGGCCTG | GCCCTGCTGT | CGGAAGCTGT | CCTGCGGGGC | 480 |
| CAGGCCCTGT | TGGTCAACTC | TTCCCAGCCG | TGG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|-----|
| CTTCGGGGCTC | TGGGAGCCCA | GAAGGAAGCC | ATCTCCCCCTC | CAGATGCGGC | CTCAGCTGCT | 60 |
| CCACTCCGAA | CAATCACTGC | TGACACTTTC | CGCAAACCTCT | TCCGAGTCTA | CTCCAATTTC | 120 |
| CTCCGGGGAA | AGCTGAAGCT | GTACACAGGG | GAGGCCTGCA | GGACAGGGGA | CAGATGAGGC | 180 |
| GGCGGCTCCC | CCCACCACGC | CTCATCTGTG | ACAGCCGAGT | CCTGGAGAGG | TACCTCTTGG | 240 |
| AGGCCAAGGA | GGCCGAGAAT | ATCACGACGG | GCTGTGCTGA | ACACTGCAGC | TTGAATGAGA | 300 |
| ATAATCACTG | TCCCAGACAC | CAAAGTTAAT | TTCTATGCCCT | GGAAGAGGAT | GGAGGTCGGG | 360 |
| CAGCAGGCCG | TAGAAGTCTG | GCAGGGCCTG | GCCCTGCTGT | CGGAAGCTGT | CCTGCGGGGC | 420 |
| CAGGCCCTGT | TGGTCAACTC | TTCCCAGCCG | TGGGAGCCCC | TGCAGCTGCA | TGTGGATAAA | 480 |
| CCGCTCAGTG | GCCTTCGCAG | CCTCACCCT | CTG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

| | | | | | | |
|------------|-------------|------------|------------|------------|------------|-----|
| CGGGCTCTTG | GAGCCCAGAA | GGAAGCCATC | TCCCCTCCAG | ATGCGGCCTC | AGCTGCTCCA | 60 |
| CTCCGAACAA | TCACTGCTGA | CACTTTCCGC | AAACTCTTCC | GAGTCTACTC | CAATTTCCTC | 120 |
| CGGGGAAAGC | TGAAGCTGTA | CACAGGGGAG | GCCTGCAGGA | CAGGGGACAG | ATGAGGCGGC | 180 |
| GGCTCCCCC | ACCACGCCCTC | ATCTGTGACA | GCCGAGTCCT | GGAGAGGTAC | CTCTTGAGAG | 240 |
| CCAAGGAGGC | CGAGAATATC | ACGACGGGCT | GTGCTGAACA | CTGCAGCTTG | AATGAGAATA | 300 |
| ATCACTGTCC | CAGACACCAA | AGTTAATTTC | TATGCCTGGA | AGAGGATGGA | GGTCGGGCAG | 360 |
| CAGCCCGTAG | AAGTCTGGCA | GGGCCTGGCC | CTGTGTCCGG | AAGCTGTCCT | GCGGGGCCAG | 420 |
| GCCCTGTTGG | TCAACTCTTC | CCAGCCGTGG | AGCCCCCTGC | AGCTGCATGT | GGATAAAGCC | 480 |
| GTCAGTGGCC | TTGCGAGCCT | CACCACTCTG | CTT | | | 513 |

(2) INFORMATION FOR SEQ ID NO:98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCTCTGGGAG | CCCAGAAGGA | AGCCATCTCC | CCTCCAGATG | CGGCCTCAGC | TGCTCCACTC | 60 |
| CGAACAATCA | CTGCTGACAC | TTTCCGCAAA | CTCTTCCGAG | TCTACTCCAA | TTTCTCCGG | 120 |

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GGAAAGCTGA | AGCTGTACAC | AGGGGAGGCC | TGCAGGACAG | GGGACAGATG | AGGCGGCGGC | 180 |
| TCCCCCACC | ACGCCTCATC | TGTGACAGCC | GAGTCCTGGA | GAGGTACCTC | TTGGAGGCCA | 240 |
| AGGAGGCCGA | GAATATCAG | ACGGGCTGTG | CTGAACACTG | CAGCTTGAAT | GAGAAATAATC | 300 |
| ACTGTCCCAG | ACACCAAAGT | TAATTTCTAT | GCCTGGAAGA | GGATGGAGGT | CGGGCAGCAG | 360 |
| GCCGTAGAAG | TCTGGCAGGG | CCTGGCCCTG | CTGTGCGAAG | CTGTCTGCG | GGGCCAGGCC | 420 |
| CTGTTGGTCA | ACTCTTCCCA | GCCGTGGGAG | CCCCTGCAGC | TGCATGTGGA | TAAAGCCGTC | 480 |
| AGTGCCTTC | GCAGCCTCAC | CACTCTGCTT | CGG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CTGGGAGCCC | AGAAGGAAGC | CATCTCCCCT | CCAGATGCGG | CCTCAGCTGC | TCCACTCCGA | 60 |
| ACAACTACTG | CTGACACTTT | CCGCAAATC | TTCCGAGTCT | ACTCCAATTT | CCTCCGGGGA | 120 |
| AAGCTGAAGC | TGTACACAGG | GGAGGCCCTG | AGGACAGGGG | ACAGATGAGG | CGGCCGCTCC | 180 |
| CCCCACCACG | CCTCATCTGT | GACAGCCGAG | TCCTGGAGAG | GTACCTCTTG | GAGGCCAAGG | 240 |
| AGGCCGAGAA | TATCACGACG | GGCTGTGCTG | AACACTGCAG | CTTGAATGAG | AATAATCACT | 300 |
| GTCCCAGACA | CCAAAGTTAA | TTTCTATGCC | TGGAAGAGGA | TGGAGGTCGG | GCAGCAGGCC | 360 |
| GTAGAAGTCT | GGCAGGGCGT | GGCCCTGCTG | TCGGAAGCTG | TCCTGCGGGG | CCAGGCCCTG | 420 |
| TTGGTCAACT | CTTCCAGGCC | GTGGGAGCCC | CTGCAGCTGC | ATGTGGATAA | AGCCGTCAGT | 480 |
| GGCCTTCGCA | GCCTCACCAC | TCTGCTTCGG | GTC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

| | | | | | | |
|------------|------------|-------------|-------------|-------------|------------|-----|
| GGAGCCCAGA | AGGAAGCCAT | CTCCCCCTCCA | GATGCGGCC'T | CAGCTGCTCC | ACTCCGAACA | 60 |
| ATCACTGCTG | ACACTTTCCG | CAAACCTTTC | CGAGTCTACT | CCAATTTCCCT | CCGGGGAAAG | 120 |
| CTGAAGCTGT | ACACAGGGGA | GGCCTGCAGG | ACAGGGGACA | GATGAGGCGG | CGGCTCCCCC | 180 |
| CACCACGCCT | CATCTGTGAC | AGCCGAGTCC | TGGAGAGGTA | CCTCTTGGAG | GCCAAGGAGG | 240 |
| CCGAGAATAT | CACGACGGGC | TGTGCTGAAC | ACTGCAGCTT | GAATGAGAAT | AATCACTGTC | 300 |
| CCAGACACCA | AAGTTAATTT | CTATGCCCTGG | AAGAGGATGG | AGGTCGGGCA | GCAGGCCGTA | 360 |
| GAAGTCTGGC | AGGGCTGGC | CCTGCTGTGC | GAAGCTGTCC | TGCGGGGCCA | GGCCCTGTTG | 420 |
| GTCAACTCTT | CCCAGCCGTG | GGAGCCCCTG | CAGCTGCATG | TGGATAAAGC | CGTCAGTGGC | 480 |
| CTTCGCAGCC | TCACCACTCT | GCTTCGGGCT | CTG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| GGCCAGAAGG | AAGCCATCTC | CCCTCCAGAT | GCGGCCTCAG | CTGCTCCACT | CCGAACAATC | 60 |
| ACTGCTGACA | CTTTCCGCAA | ACTCTTCCGA | GTCTACTCCA | ATTTCTCTCCG | GGGAAAGCTG | 120 |
| AAGTGTGACA | CAGGGGAGGC | CTGCAGGACA | GGGGACAGAT | GAGGCGGCGG | CTCCCCCAC | 180 |
| CACGCCTCAT | CTGTGACAGC | CGAGTCCTGG | AGAGGTACCT | CTTGGAGGCC | AAGGAGGCCG | 240 |
| AGAATATCAC | GACGGGCTGT | GCTGAACACT | GCAGCTTGAA | TGAGAATAAT | CACTGTCCCA | 300 |
| GACACCAAAG | TTAATTTCTA | TGCCTGGAAG | AGGATGGAGG | TCGGGCAGCA | GGCCGTAGAA | 360 |
| GTCTGGCAGG | GCCTGGCCCT | GCTGTGCGAA | GCTGTCTGTC | GGGGCCAGGC | CCTGTGGTCT | 420 |
| AACTCTTCCC | AGCCGTGGGA | GCCCCTGCAG | CTGCATGTGG | ATAAAGCCGT | CAGTGGCCTT | 480 |
| CGCAGCCTCA | CCACTCTGCT | TCGGGCTCTG | GGA | | | 513 |

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CAGAAGGAAG | CCATCTCCCC | TCCAGATGCG | GCCTCAGCTG | CTCCACTCCG | AACAATCACT | 60 |
| GCTGACACTT | TCCGCAAACT | CTTCCGAGTC | TACTCCAATT | TCCTCCGGGG | AAAGCTGAAG | 120 |
| CTGTACACAG | GGGAGGCCTG | CAGGACAGGG | GACAGATGAG | GCGGCGGCTC | CCCCACCAC | 180 |
| GCCTCATCTG | TGACAGCCGA | GTCCTGGAGA | GGTACCTCTT | GGAGGCCAAG | GAGGCCGAGA | 240 |
| ATATCACGAC | GGGCTGTGCT | GAACACTGCA | GCTTGAATGA | GAATAATCAC | TGTCCCAGAC | 300 |
| ACCAAAGTTA | ATTTCTATGC | CTGGAAGAGG | ATGGAGGTCG | GGCAGCAGGC | CGTAGAAGTC | 360 |
| TGGCAGGGCC | TGGCCCTGCT | GTCGGAAGCT | GTCCTGCGGG | GCCAGGCCCT | GTTGGTCAAC | 420 |
| TCTTCCAGC | CGTGGGAGCC | CCTGCAGCTG | CATGTGGATA | AAGCCGTCAG | TGGCCTTCGC | 480 |
| AGCCTCACCA | CTCTGCTTCG | GGCTCTGGGA | GCC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| AAGGAAGCCA | TCTCCCTCC | AGATGCGGCC | TCAGCTGCTC | CACTCCGAAC | AATCACTGCT | 60 |
| GACACTTTCC | GCAAACCTT | CCGAGTCTAC | TCCAATTTCC | TCCGGGGAAA | GCTGAAGCTG | 120 |
| TACACAGGGG | AGGCTGCGAG | GACAGGGGAC | AGATGAGGCG | GCGGCTCCCC | CCACCACGCC | 180 |
| TCATCTGTGA | CAGCCGAGTC | CTGGAGAGGT | ACCTCTTGGA | GGCCAAGGAG | GCCGAGAATA | 240 |
| TCACGACGGG | CTGTGCTGAA | CACTGCAGCT | TGAATGAGAA | TAATCACTGT | CCCAGACACC | 300 |
| AAAGTTAATT | TCTATGCCTG | GAAGAGGATG | GAGGTCGGGC | AGCAGGCCGT | AGAAGTCTGG | 360 |
| CAGGGCCTGG | CCCTGCTGTC | GGAAGCTGTC | CTGCGGGGCC | AGGCCCTGTT | GGTCAACTCT | 420 |
| TCCAGCCCGT | GGGAGCCCT | GCAGCTGCAT | GTGGATAAAG | CCGTCAGTGG | CCTTCGCAGC | 480 |
| CTCACCACTC | TGCTTCGGGC | TCTGGGAGCC | CAG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| GAAGCCATCT | CCCCTCCAGA | TGCGGCCTCA | GCTGCTCCAC | TCCGAACAAT | CACTGCTGAC | 60 |
| ACTTTCCGCA | AACTCTTCCG | AGTCTACTCC | AATTTCTCTC | GGGGAAAGCT | GAAGCTGTAC | 120 |
| ACAGGGGAGG | CCTGCAGGAC | AGGGGACAGA | TGAGGCGGCG | GCTCCCCCA | CCACGCCTCA | 180 |
| TCTGTGACAG | CCGAGTCTCT | GAGAGGTACC | TCTTGGAGGC | CAAGGAGGCC | GAGAAATATCA | 240 |
| CGACGGGCTG | TGCTGAACAC | TGCAGCTTGA | ATGAGAATAA | TCACTGTCCC | AGACACCAAA | 300 |
| GTTAATTTCT | ATGCCGTGAA | GAGGATGGAG | GTGCGGCAGC | AGGCCGTAGA | AGTCTGGCAG | 360 |
| GGCTGGCCCC | TGCTGTCGGA | AGCTGTCTCT | CGGGGCCAGG | CCCTGTTGGT | CAACTCTTCC | 420 |
| CAGCCGTGGG | AGCCCTTGCA | GCTGCATGTG | GATAAAGCCG | TCAGTGGCCT | TCGCAGCCTC | 480 |
| ACCACCTCTG | TTGCGGCTCT | GGGAGCCAG | AAG | | | 513 |

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

| | | | | | | |
|-------------|------------|------------|------------|------------|------------|-----|
| GCCATCTCCC | CTCCAGATGC | GGCCTCAGCT | GCTCCACTCC | GAACAATCAC | TGCTGACACT | 60 |
| TTCCGCAAAAC | TCCTCCGAGT | CTACTCCAAT | TTCTTCCGGG | GAAAGCTGAA | GCTGTACACA | 120 |
| GGGGAGGCCT | GCAGGACAGG | GGACAGATGA | GGCGGCGGCT | CCCCCACCA | CGCTCATCT | 180 |
| GTGACAGCCG | AGTCTTGGAG | AGGTACCTCT | TGGAGGCCAA | GGAGGCCGAG | AATATCACGA | 240 |
| CGGGCTGTGC | TGAACACTGC | AGCTTGAATG | AGAATAATCA | CTGTCCCAGA | CACCAAAGTT | 300 |
| AATTTCTATG | CCTGGAAGAG | GATGGAGGTC | GGGCAGCAGG | CCGTAGAAGT | CTGGCAGGGC | 360 |
| CTGGCCCTGC | TGTCGGAAGC | TGTCCTGCGG | GGCCAGGCC | TGTTGGTCAA | CTCTTCCAG | 420 |
| CCGTGGGAGC | CCCTGCAGCT | GCATGTGGAT | AAAGCCGTCA | GTGGCCTTCG | CAGCCTCACC | 480 |
| ACTCTGCTTC | GGGCTCTGGG | AGCCAGAAAG | GAA | | | 513 |

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(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ATCTCCCTC | CAGATGCGGC | CTCAGCTGCT | CCACTCCGAA | CAATCACTGC | TGACACTTTC | 60 |
| CGCAAACCT | TCCGAGTCTA | CTCCAATTTC | CTCCGGGGAA | AGCTGAAGCT | GTACACAGGG | 120 |
| GAGGCCTGCA | GGACAGGGGA | CAGATGAGGC | GGCGGCTCCC | CCCACCACGC | CTCATCTGTG | 180 |
| ACAGCCGAGT | CCTGGAGAGG | TACCTCTTGG | AGGCCAAGGA | GGCCGAGAAT | ATCACGACGG | 240 |
| GCTGTGCTGA | ACACTGCAGC | TTGAATGAGA | ATAATCACTG | TCCCAGACAC | CAAAGTTAAT | 300 |
| TTCTATGCCT | GGAAGAGGAT | GGAGGTCGGG | CAGCAGGCCG | TAGAAGTCTG | GCAGGGCCTG | 360 |
| GCCCTGCTGT | CGGAAGCTGT | CCTGCGGGGC | CAGGCCCTGT | TGGTCAACTC | TTCCCAGCCG | 420 |
| TGGGAGCCCC | TGCAGTGCA | TGTGGATAAA | GCCGTCAGTG | GCCTTCGCAG | CCTCACCCT | 480 |
| CTGCTTCGGG | CTCTGGGAGC | CCAGAAGGAA | GCC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| TCCCTCCAG | ATGCGGCCTC | AGCTGCTCCA | CTCCGAACAA | TCACTGCTGA | CACTTTCGCG | 60 |
| AAACTCTTCC | GAGTCTACTC | CAATTTCCCTC | CGGGGAAAGC | TGAAGCTGTA | CACAGGGGAG | 120 |
| GCCTGCAGGA | CAGGGGACAG | ATGAGGCGGC | GGCTCCCCC | ACCACGCCTC | ATCTGTGACA | 180 |
| GCCGAGTCCT | GGAGAGGTAC | CTCTTGGAGG | CCAAGGAGGC | CGAGAATATC | ACGACGGGCT | 240 |
| GTGTGAACA | CTGCAGCTTG | AATGAGAATA | ATCACTGTCC | CAGACACCAA | AGTTAATTTT | 300 |
| TATGCTTGGA | AGAGGATGGA | GGTCGGGCAG | CAGGCCGTAG | AAGTCTGGCA | GGGCTGGCC | 360 |
| CTGTGTCGG | AAGCTGTCTT | GCGGGGCCAG | GCCCTGTTGG | TCAACTCTTC | CCAGCCGTGG | 420 |
| GAGCCCTGC | AGCTGCATGT | GGATAAAGCC | GTCAGTGGCC | TTGCGAGCCT | CACCACTCTG | 480 |
| CTTCGGGCTC | TGGGAGCCCA | GAAGGAAGCC | ATC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCTCCAGATG | CGGCCTCAGC | TGCTCCACTC | CGAACAATCA | CTGCTGACAC | TTTCCGCAAA | 60 |
| CTCTTCCGAG | TCTACTCCAA | TTTCCTCCGG | GGAAAGCTGA | AGCTGTACAC | AGGGGAGGCC | 120 |
| TGCAGGACAG | GGGACAGATG | AGGCGGCGGC | TCCCCCACC | ACGCCTCATC | TGTGACAGCC | 180 |
| GAGTCCTGGA | GAGGTACCTC | TTGGAGGCCA | AGGAGGCCGA | GAATATCACG | ACGGGCTGTG | 240 |
| CTGAACACTG | CAGCTTGAAT | GAGAATAATC | ACTGTCCCAG | ACACCAAAGT | TAATTTCTAT | 300 |
| GCCTGGAAGA | GGATGGAGGT | CGGGCAGCAG | GCCGTAGAAG | TCTGGCAGGG | CCTGGCCCTG | 360 |
| CTGTGCGAAG | CTGTCTTGCG | GGGCCAGGCC | CTGTTGGTCA | ACTCTTCCCA | GCCGTGGGAG | 420 |
| CCCCTGACAG | TGCATGTGGA | TAAAGCCGTC | AGTGGCCTTC | GCAGCCTCAC | CACTCTGCTT | 480 |
| GCGGCTCTGG | GAGCCAGAA | GGAAGCCATC | TCC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| CCAGATGCGG | CCTCAGCTGC | TCCACTCCGA | ACAATCACTG | CTGACACTTT | CCGAAACTC | 60 |
| TTCCGAGTCT | ACTCCAATTT | CCTCCGGGGA | AAGCTGAAGC | TGTACACAGG | GGAGGCCTGC | 120 |

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AGGACAGGGG ACAGATGAGG CGGCGGCTCC CCCCACCACG CCTCATCTGT GACAGCCGAG 180
 TCCTGGAGAG GTACCTCTTG GAGGCCAAGG AGGCCGAGAA TATCACGACG GGCTGTGCTG 240
 AACACTGCAG CTTGAATGAG AATAATCACT GTCCCAGACA CCAAAGTTAA TTTCTATGCC 300
 TGGAGAGGTA TGGAGGTCGG GCAGCAGGCC GTAGAAGTCT GGCAGGGCCT GGCCCTGCTG 360
 TCGGAAGCTG TCCTGCGGGG CCAGGCCCTG TTGGTCAACT CTTCCCAGCC GTGGGAGCCC 420
 CTGCAGCTGC ATGTGGATAA AGCCGTCAGT GGCCTTCGCA GCCTCACCAC TCTGCTTCGG 480
 GCTCTGGGAG CCCAGAAGGA AGCCATCTCC CCT 513

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GATGCGGCCT CAGCTGCTCC ACTCCGAACA ATCACTGCTG ACACCTTCCG CAACTCTTC 60
 CGAGTCTACT CCAATTTCCT CCGGGGAAAG CTGAAGCTGT ACACAGGGGA GGCTGCAGG 120
 ACAGGGGACA GATGAGGCGG CGGCTCCCCC CACCACGCC TATCTGTGAC AGCCGAGTCC 180
 TGGAGAGGTA CCTCTTGAGG GCCAAGGAGG CCGAGAATAT CACGACGGGC TGTGCTGAAC 240
 ACTGCAGCTT GAATGAGAAT AATCACTGTC CCAGACACCA AAGTTAATTT CTATGCCTGG 300
 AAGAGGATGG AGGTCGGGCA GCAGGCCGTA GAAGTCTGGC AGGGCCTGGC CCTGCTTCG 360
 GAAGCTGTCC TCGGGGGCCA GGCCCTGTTG GTCAACTCTT CCCAGCCGTG GGAGCCCTG 420
 CAGCTGCATG TGGATAAAGC CGTCAGTGGC CTTGCGAGCC TCACCACTCT GCTTCGGGCT 480
 CTGGGAGCCC AGAAGGAAGC CATCTCCCTT CCA 513

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

GCGGCCTCAG CTGCTCCACT CCGAACAATC ACTGCTGACA CTTTCCGCAA ACTCTTCCGA 60
 GTCTACTCCA ATTTCTCCG GGGAAAGCTG AAGCTGTACA CAGGGGAGGC CTGCAGGACA 120
 GGGGACAGAT GAGGCGGCGG CTCCCCCACC CACGCCTCAT CTGTGACAGC CGAGTCTTGG 180
 AGAGGTACCT CTTGGAGGCC AAGGAGGCCG AGAATATCAC GACGGGCTGT GCTGAACACT 240
 GCAGCTTGAA TGAGAATAAT CACTGTCCCA GACACCAAAG TTAATTTCTA TGCCTGGAAG 300
 AGGATGGAGG TCGGGCAGCA GGCCGTAGAA GTCTGGCAGG GCCTGGCCCT GCTGTCGGAA 360
 GCTGTCCTGC GGGGCCAGGC CCTGTTGGTC AACTCTTCCC AGCCGTGGGA GCCCTGCAG 420
 CTGCATGTGG ATAAAGCCGT CAGTGGCCTT CGCAGCCTCA CCACTCTGCT TCGGGCTCTG 480
 GGAGCCCAGA AGGAAGCCAT CTCCCCCCA GAT 513

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

GCCTCAGCTG CTCCAATCCG AACAACTCACT GCTGACACTT TCCGCAAACCT CTTCCGAGTC 60
 TACTCCAATT TCCTCCGGGG AAAGCTGAAG CTGTACACAG GGGAGGCCTG CAGGACAGGG 120
 GACAGATGAG GCGGCGGCTC CCCCACCAC GCCTCATCTG TGACAGCCGA GTCTGGAGA 180
 GGTACCTCTT GGAGGCCAAG GAGGCCGAGA ATATCACGAC GGGCTGTGCT GAACACTGCA 240
 GCTTGAATGA GAATAATCAC TGTCCAGAC ACCAAAGTTA ATTTCTATGC CTGGAAGAGG 300
 ATGGAGGTCG GGCAGCAGGC CGTAGAAGTC TGGCAGGGCC TGGCCCTGCT GTCGGAAGCT 360
 GTCTGCGGG GCCAGCCCT GTTGGTCAAC TCTTCCCAGC CGTGGGAGCC CCTGCAGCTG 420
 CATGTGGATA AAGCCGTCAG TGGCCTTCGC AGCCTACCA CTCTGCTTCG GGCTCTGGGA 480
 GCCCAGAAGG AAGCCATCTC CCCTCAGAT GCG 513

(2) INFORMATION FOR SEQ ID NO:113:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

| | | | | | | |
|------------|------------|------------|------------|-------------|------------|-----|
| TCAGCTGCTC | CACTCCGAAC | AATCACTGCT | GACACTTTCC | GCAAACCTCTT | CCGAGTCTAC | 60 |
| TCCAATTTCC | TCCGGGGAAA | GCTGAAGCTG | TACACAGGGG | AGGCCTGCAG | GACAGGGGAC | 120 |
| AGATGAGGCG | GCGGCTCCCC | CCACCACGCC | TCATCTGTGA | CAGCCGAGTC | CTGGAGAGGT | 180 |
| ACCTCTTGGA | GGCCAAGGAG | GCCGAGAATA | TCACGACGGG | CTGTGCTGAA | CACTGCAGCT | 240 |
| TGAATGAGAA | TAATCACTGT | CCCAGACACC | AAAGTTAATT | TCTATGCCTG | GAAGAGGATG | 300 |
| GAGGTCCGGC | AGCAGGCCGT | AGAAGTCTGG | CAGGGCCTGG | CCCTGCTGTC | GGAAGCTGTC | 360 |
| CTGCGGGGCC | AGGCCCTGTT | GGTCAACTCT | TCCCAGCCGT | GGGAGCCCCT | GCAGCTGCAT | 420 |
| GTGGATAAAG | CCGTCACTGG | CCTTCGCAGC | CTCACCACCT | TGCTTCGGGC | TCTGGGAGCC | 480 |
| CAGAAGGAAG | CCATCTCCCC | TCCAGATGCG | GCC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

| | | | | | | |
|------------|------------|-------------|------------|------------|------------|-----|
| GCTGCTCCAC | TCCGAACAAT | CACTGCTGAC | ACTTTCGCCA | AACTCTTCCG | AGTCTACTCC | 60 |
| AATTTCCTCC | GGGGAAAGCT | GAAGCTGTAC | ACAGGGGAGG | CCTGCAGGAC | AGGGGACAGA | 120 |
| TGAGGCGGCG | GCTCCCCCCA | CCACGCCCTCA | TCTGTGACAG | CCGAGTCCTG | GAGAGGTACC | 180 |
| TCTTGAGGCG | CAAGGAGGCC | GAGAATATCA | CGACGGGCTG | TGCTGAACAC | TGCAGCTTGA | 240 |
| ATGAGAATAA | TCACTGTCCC | AGACACCAAA | GTTAATTTCT | ATGCCTGGAA | GAGGATGGAG | 300 |
| GTCCGGCAGC | AGGCCGTAGA | AGTCTGGCAG | GGCCTGGCCC | TGCTGTCCGA | AGCTGTCTTG | 360 |
| CGGGGCCAGG | CCCTGTTGGT | CAACTCTTCC | CAGCCGTGGG | AGCCCCTGCA | GCTGCATGTG | 420 |
| GATAAAGCCG | TCAGTGGCCT | TGCGAGCCTC | ACCACTCTGC | TTCCGGCTCT | GGGAGCCAG | 480 |
| AAGGAAGCCA | TCTCCCTTCC | AGATGCGGCC | TCA | | | 513 |

(2) INFORMATION FOR SEQ ID NO:115:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCTCCACTCC | GAACAATCAC | TGCTGACACT | TTCCGCAAAC | TCTTCCGAGT | CTACTCCAAT | 60 |
| TTCCCTCCGG | GAAAGCTGAA | GCTGTACACA | GGGGAGCCCT | GCAGGACAGG | GGACAGATGA | 120 |
| GGCGGCGGCT | CCCCCACCA | CGCCTCATCT | GTGACAGCCG | AGTCCTGGAG | AGGTACCTCT | 180 |
| TGGAGGCCAA | GGAGGCCGAG | AATATCACGA | CGGGCTGTGC | TGAACACTGC | AGCTTGAATG | 240 |
| AGAATAATCA | CTGTCCCAGA | CACCAAAGTT | AATTTCTATG | CCTGGAAGAG | GATGGAGGTC | 300 |
| GGGCAGCAGG | CCGTAGAAGT | CTGGCAGGGC | CTGGCCCTGC | TGTCGGAAGC | TGTCCTGCGG | 360 |
| GGCCAGGCCC | TGTTGGTCAA | CTCTTCCCAG | CCGTGGGAGC | CCCTGCAGCT | GCATGTGGAT | 420 |
| AAAGCCGTCA | GTGGCCTTCG | CAGCCTCACC | ACTCTGCTTC | GGGCTCTGGG | AGCCCAGAAG | 480 |
| GAAGCCATCT | CCCCCTCAGA | TGCGGCCTCA | GCT | | | 513 |

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

| | | | | | | |
|------------|------------|------------|-------------|------------|-------------|-----|
| CCACTCCGAA | CAATCACTGC | TGACACTTTC | CGCAAACCTCT | TCCGAGTCTA | CTCCAATTTCT | 60 |
| CTCCGGGGAA | AGCTGAAGCT | GTACACAGGG | GAGGCCTGCA | GGACAGGGGA | CAGATGAGGC | 120 |
| GGCGGCTCCC | CCCACCACGC | CTCATCTGTG | ACAGCCGAGT | CCTGGAGAGG | TACCTCTTGG | 180 |
| AGGCCAAGGA | GGCCGAGAAT | ATCACGACGG | GCTGTGCTGA | ACACTGCAGC | TTGAATGAGA | 240 |
| ATAATCACTG | TCCCAGACAC | CAAAGTTAAT | TTCTATGCCT | GGAAGAGGAT | GGAGGTCGGG | 300 |
| CAGCAGGCCG | TAGAAGTCTG | GCAGGGCCTG | GCCCTGCTGT | CGGAAGCTGT | CCTGCGGGGC | 360 |
| CAGGCCTGT | TGGTCAACTC | TTCCCAGCCG | TGGGAGCCCC | TGCAGCTGCA | TGTGGATAAA | 420 |
| GCCGTCACTG | GCCTTCGCAG | CCTCACCAC | CTGCTTCGGG | CTCTGGGAGC | CCAGAAGGAA | 480 |
| GCCATCTCCC | CTCCAGATGC | GGCCTCAGCT | GCT | | | 513 |

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

| | | | | | | |
|-------------|------------|------------|------------|------------|-------------|-----|
| CTCCGAACAA | TCACGTCTGA | CACTTTCCGC | AAACTCTTCC | GAGTCTACTC | CAATTTCCCTC | 60 |
| CGGGGAAAGC | TGAAGCTGTA | CACAGGGGAG | GCCTGCAGGA | CAGGGGACAG | ATGAGGCGGC | 120 |
| GGCTCCCCC | ACCAGCCTC | ATCTGTGACA | GCCGAGTCCT | GGAGAGGTAC | CTCTTGGAGG | 180 |
| CCAAGGAGGC | CGAGAATATC | ACGACGGGCT | GTGCTGAACA | CTGCAGCTTG | AATGAGAATA | 240 |
| ATCACTGTCC | CAGACACCAA | AGTTAATTTC | TATGCCTGGA | AGAGGATGGA | GGTCGGGCAG | 300 |
| CAGGCCGTAG | AAGTCTGGCA | GGGCCTGGCC | CTGCTGTCCG | AAGCTGTCTC | GCGGGGCCAG | 360 |
| GCCCTGTTGG | TCAACTCTTC | CCAGCCGTGG | GAGCCCCCTG | AGCTGCATGT | GGATAAAGCC | 420 |
| GTCAGTGGCC | TTCGCAGCCT | CACCACTCTG | CTTCGGGCTC | TGGGAGCCCA | GAAGGAAGCC | 480 |
| ATCTCCCCCTC | CAGATGCGGC | CTCAGCTGCT | CCA | | | 513 |

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

| | | | | | | |
|------------|------------|------------|------------|------------|-------------|-----|
| CGAACAATCA | CTGCTGACAC | TTTCCGCAAA | CTCTTCCGAG | TCTACTCCAA | TTTCCTCCGG | 60 |
| GGAAAGCTGA | AGCTGTACAC | AGGGGAGGCC | TGCAGGACAG | GGGACAGATG | AGGCGGCGGC | 120 |
| TCCCCCACC | ACGCCTCATC | TGTGACAGCC | GAGTCCTGGA | GAGGTACCTC | TTGGAGGCCA | 180 |
| AGGAGGCCGA | GAATATCAG | ACGGGCTGTG | CTGAACACTG | CAGCTTGAAT | GAGAAATAATC | 240 |
| ACTGTCCCAG | ACACCAAAGT | TAATTTCTAT | GCCTGGAAGA | GGATGGAGGT | CGGGCAGCAG | 300 |
| GCCGTAGAAG | TCTGGCAGGG | CCTGGCCCTG | CTGTCGGAAG | CTGTCTGCG | GGGCCAGGCC | 360 |
| CTGTTGGTCA | ACTCTTCCCA | GCCGTGGGAG | CCCCTGCAGC | TGCATGTGGA | TAAAGCCGTC | 420 |
| AGTGGCCTTC | GCAGCTCAC | CACTCTGCTT | CGGGCTCTGG | GAGCCCAGAA | GGAAGCCATC | 480 |
| TCCCCTCCAG | ATGCGGCCTC | AGCTGCTCCA | CTC | | | 513 |

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 513 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| ACAATCACTG | CTGACACTTT | CCGCAAACCT | TTCCGAGTCT | ACTCCAATTT | CCTCCGGGGA | 60 |
| AAGCTGAAGC | TGTACACAGG | GGAGGCCTGC | AGGACAGGGG | ACAGATGAGG | CGGCGGCTCC | 120 |
| CCCCACCACG | CCTCATCTGT | GACAGCCGAG | TCCTGGAGAG | GTACCTCTTG | GAGGCCAAGG | 180 |
| AGGCCGAGAA | TATCACGACG | GGCTGTGCTG | AACACTGCAG | CTTGAATGAG | AATAATCACT | 240 |
| GTCCCAGACA | CCAAAGTTAA | TTTCTATGCC | TGGAAGAGGA | TGGAGGTCGG | GCAGCAGGCC | 300 |
| GTAGAAGTCT | GGCAGGGCCT | GGCCCTGCTG | TCGGAAGCTG | TCCTGCGGGG | CCAGGCCCTG | 360 |
| TTGTGCAACT | CTTCCCAGCC | GTGGGAGCCC | CTGCAGCTGC | ATGTGGATAA | AGCCGTCAGT | 420 |
| GGCCTTCGCA | GCCTCACCAC | TCTGCTTCGG | GCTCTGGGAG | CCCAGAAGGA | AGCCATCTCC | 480 |
| CCTCCAGATG | CGGCCTCAGC | TGCTCCACTC | CGA | | | 513 |

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

| | | | | | | |
|------------|------------|------------|------------|------------|------------|-----|
| GCCCCACCAC | GCCTCATCTG | TGACAGCCGA | GTCTTGAGAG | GGTACCTCTT | GGAGGCCAAG | 60 |
| GAGGCCGAGA | ATATCACGAC | GGGCTGTGCT | GAACACTGCA | GCTTGAATGA | GAATATCACT | 120 |

GTCCCAGACA CCAAAGTTAA TTTCTATGCC TGGGAAGAGGA TGGAGGTCGG GCAGCAGGCC 180
 GTAGAAGTCT GGCAGGGCCT GGCCCTGCTG TCGGAAGCTG TCCTGCGGGG CCAGGCCCTG 240
 TTGGTCAACT CTTCCAGCC GTGGGAGCCC CTGCAGCTGC ATGTGGATAA AGCCGTCAGT 300
 GGCCCTTCGCA GCCTCACCAC TCTGCTTCGG GCTCTGGGAG CCCAGAAGGA AGCCATCTCC 360
 CCTCCAGATG CGGCCTCAGC TGCTCCACTC CGAACAATCA CTGCTGACAC TTTCCGCAAA 420
 CTCTTCCGAG TCTACTCCAA TTTCTCCCGG GGAAAGCTGA AGCTGTACAC AGGGGAGGCC 480
 TGCAGGACAG GGGACAGATG A 501

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Ala | Pro | Pro | Arg | Leu | Ile | Cys | Asp | Ser | Arg | Val | Leu | Glu | Arg | Tyr | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Leu | Glu | Ala | Lys | Glu | Ala | Glu | Asn | Ile | Thr | Thr | Gly | Cys | Ala | Glu | His |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Cys | Ser | Leu | Asn | Glu | Asn | Ile | Thr | Val | Pro | Asp | Thr | Lys | Val | Asn | Phe |
| | | 35 | | | | | 40 | | | | | 45 | | | |
| Tyr | Ala | Trp | Lys | Arg | Met | Glu | Val | Gly | Gln | Gln | Ala | Val | Glu | Val | Trp |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Gln | Gly | Leu | Ala | Leu | Leu | Ser | Glu | Ala | Val | Leu | Arg | Gly | Gln | Ala | Leu |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |
| Leu | Val | Asn | Ser | Ser | Gln | Pro | Trp | Glu | Pro | Leu | Gln | Leu | His | Val | Asp |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Lys | Ala | Val | Ser | Gly | Leu | Arg | Ser | Leu | Thr | Thr | Leu | Leu | Arg | Ala | Leu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Gly | Ala | Gln | Lys | Glu | Ala | Ile | Ser | Pro | Pro | Asp | Ala | Ala | Ser | Ala | Ala |
| | | 115 | | | | | 120 | | | | 125 | | | | |
| Pro | Leu | Arg | Thr | Ile | Thr | Ala | Asp | Thr | Phe | Arg | Lys | Leu | Phe | Arg | Val |
| | 130 | | | | 135 | | | | | | 140 | | | | |
| Tyr | Ser | Asn | Phe | Leu | Arg | Gly | Lys | Leu | Lys | Leu | Tyr | Thr | Gly | Glu | Ala |
| 145 | | | | 150 | | | | | | 155 | | | | | 160 |
| Cys | Arg | Thr | Gly | Asp | Arg | | | | | | | | | | |
| | | | | 165 | | | | | | | | | | | |

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Thr | Val | Pro | Asp | Thr | Lys | Val | Asn | Phe | Tyr | Ala | Trp | Lys | Arg | Met | Glu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Gly | Gln | Gln | Ala | Val | Glu | Val | Trp | Gln | Gly | Leu | Ala | Leu | Leu | Ser |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Ala | Val | Leu | Arg | Gly | Gln | Ala | Leu | Leu | Val | Asn | Ser | Ser | Gln | Pro |
| | | 35 | | | | | 40 | | | | 45 | | | | |
| Trp | Glu | Pro | Leu | Gln | Leu | His | Val | Asp | Lys | Ala | Val | Ser | Gly | Leu | Arg |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Ser | Leu | Thr | Thr | Leu | Leu | Arg | Ala | Leu | Gly | Ala | Gln | Lys | Glu | Ala | Ile |
| 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Ser | Pro | Pro | Asp | Ala | Ala | Ser | Ala | Ala | Pro | Leu | Arg | Thr | Ile | Thr | Ala |
| | | | 85 | | | | | 90 | | | | | 95 | | |
| Asp | Thr | Phe | Arg | Lys | Leu | Phe | Arg | Val | Tyr | Ser | Asn | Phe | Leu | Arg | Gly |
| | | | 100 | | | | | 105 | | | | 110 | | | |
| Lys | Leu | Lys | Leu | Tyr | Thr | Gly | Glu | Ala | Cys | Arg | Thr | Gly | Asp | Arg | Gly |
| | | 115 | | | | | 120 | | | | 125 | | | | |
| Gly | Gly | Ser | Ala | Pro | Pro | Arg | Leu | Ile | Cys | Asp | Ser | Arg | Val | Leu | Glu |
| | 130 | | | | 135 | | | | | | 140 | | | | |
| Arg | Tyr | Leu | Leu | Glu | Ala | Lys | Glu | Ala | Glu | Asn | Ile | Thr | Thr | Gly | Cys |
| 145 | | | | 150 | | | | | | 155 | | | | | 160 |
| Ala | Glu | His | Cys | Ser | Leu | Asn | Glu | Asn | Ile | | | | | | |
| | | | | 165 | | | | | 170 | | | | | | |

(2) INFORMATION FOR SEQ ID NO:123:

2025-10-10 15:00:00

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Gly Gly Gly Ser

1

(2) INFORMATION FOR SEQ ID NO:124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Gly Gly Gly Ser Gly Gly Gly Ser

1

5

(2) INFORMATION FOR SEQ ID NO:125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser

1

5

10

(2) INFORMATION FOR SEQ ID NO:126:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Ser Gly Gly Ser Gly Gly Ser

1

5

(2) INFORMATION FOR SEQ ID NO:127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Glu Phe Gly Asn Met

1

5

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

"45645630"

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Glu Phe Gly Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Glu Phe Gly Gly Asn Gly Gly Asn Met
1 5

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: None

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Gly Gly Ser Asp Met Ala Gly
1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

GCGCGCCCAT GGACAATCAC TGCTGAC

27

(2) INFORMATION FOR SEQ ID NO:132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

TCTGTCCCCT GTCCT

15

(2) INFORMATION FOR SEQ ID NO:133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 43 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

267207 1564580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

GCGCGCAAGC TTATTATCGG AGTGGAGCAG CTGAGGCCGC ATC

43

(2) INFORMATION FOR SEQ ID NO:134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GCCCCACCAC GCCTCATCTG T

21

08954954 102197

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